

DRAFT

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Docket No.: 1101-209-999

Serial No.: 09/079,819

Inventor(s): ALVAREZ et al.

Title: "RANDOM PEPTIDES THAT BIND TO GASTROINTESTINAL
TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS"

20 40 60
MGMSKSHSFFGYPLSIFFIV VNEFCERFSYYGMRAILILY FTNFISWDDNLSTAIYHTFV

80 100 120
ALCYLTPILGALIADSWLGK FKTIVSLSIVYTIGQAVTSV SSINDLTDHNHDGTPDSLKV

140 160 180
HVVLSLIGLALIALGTGGIK PCVSAFGGDQFEEGQEKRQN RFFSIFYLAINAGSLLSTII

200 220 240
TPMLRVQQCGIHSKQACYPL AFGVPAALMAVALIVFVLGS GMYKKFKPQGNIMGKVAKCI

260 280 300
GFAIKNRFRHRSKAFTPKEH WLDWAKEKYDERLISQIKMV TRVMFLYIPLPMFWALFDQQ

320 340 360
GSRWTLQATTMSGKIGALEI QPDQMQTVNAILIVIMVPIF DAVLYPLIAKCGFNFTSLKK

380 400 420
MAVGMVLASMAFVVAIIVQV EIDKTLPVFPKGNEVQIKVL NIGNNTMNISLPGEMVTLGP

440 460 480
MSQTNAFMTFDVNKLTRINI SSPGSPVTAVTDDFKQGQRH TLLVWAPNHYQVVKDGLNQK

500 520 540
PEKGENGIRFVNTFNELITI TMSGKVYANISSYNASTYQF FPSGIKGFTISSTEIPPQCQ

560 580 600
PNFNTFYLEFGSAYTYIVQR KNDSCPEVKVFEDISANTVN MALQIPQYFLLTCGEVVFSV

620 640 660
TGLEFSYSQAPSNMKSVLQA GWLLTVAVGNIIVLIVAGAG QFSKQWAEYILFAALLLVVC

680 700 708
VIFAIMARFYTYINPAEIEA QFDEDEKNRLEKSNPYFMS GANSQKQM

FIG.1

1 gaattccgtc tcgaccactg aatggaagaa aaggacttt aaccaccatt ttgtgactta
61 cagaaaaggaa tttgaataaa gaaaactatg atacttcagg cccatcttca ctcccgtgt
M I L Q A H L H S L C
121 cttcttatgc tttatggc aactggatat ggccaagagg ggaagtttag tggaccctcg
L L M L Y L A T G Y G Q E G K F S G P L
181 aaacccatga cattttctat ttatgaaggc caagaaccga gtcaaattat attccagtt
K P M T F S I Y E G Q E P S Q I I F Q F
241 aaggccaatc ctccgtctgt gactttgaa ctaactgggg agacagacaa catatttg
K A N P P A V T F E L T G E T D N I F V
301 atagaacggg agggacttct gtattacaac agagccttgg acagggaaac aagatctact
I E R E G L L Y Y N R A L D R E T R S T
361 cacaatctcc aggtgcagc cctggacgct aatggaatta tagtggaggg tccagtcct
H N L Q V A A L D A N G I I V E G P V P
421 atcaccatag aagtgaagga catcaacgac aatcgaccca cgtttctcca gtcaaagtac
I T I E V K D I N D N R P T F L Q S K Y
481 gaaggctcag taaggcagaa ctctcgccca ggaaagccct tcttgtatgt caatgccaca
E G S V R Q N S R P G K P F L Y V N A T
541 gacctggatg atccggccac tcccaatggc cagcttatt accagattgt catccagctt
D L D D P A T P N G Q L Y Y Q I V I Q L
601 cccatgatca acaatgtcat gtactttcag atcaacaaca aaacgggagc catctctt
P M I N N V M Y F Q I N N K T G A I S L
661 acccgagagg gatctcagga attgaatcct gctaagaatc cttcctataa tctggtgatc
T R E G S Q E L N P A K N P S Y N L V I
721 tcagtgaagg acatggagg ccagagttag aattcccttca gtgataccac atctgtggat
S V K D M G G Q S E N S F S D T T S V D
781 atcatagtga cagagaatat ttggaaagca ccaaaacctg tggagatggt ggaaaactca
I I V T E N I W K A P K P V E M V E N S
841 actgatcctc accccatcaa aatcaactcag gtgcgggtgg atgatccccg tgcacaatat
T D P H P I K I T Q V R W N D P G A Q Y
901 tccttagttg acaaagagaa gctgccaaga ttcccatttt caattgacca ggaaggagat
S L V D K E K L P R F P F S I D Q E G D
961 atttacgtga ctacggccctt ggaccgagaa gaaaaggatg catatgtttt ttatgcgtt
I Y V T Q P L D R E E K D A Y V F Y A V
1021 gcaaaggatg agtacggaaa accacttca tatccgtgg aaattcatgt aaaagttaaa
A K D E Y G K P L S Y P L E I H V K V K
1081 gatattaatg ataatccacc tacatgtccg tcaccagtaa ccgtatttga ggtccaggag
D I N D N P P T C P S P V T V F E V Q E
1141 aatgaacgac tggtaacag tatcggtggacc cttactgcac atgacagggaa tgaagaaaaat
N E R L G N S I G T L T A H D R D E E N
1201 actgccaaca gtttctaaa ctacaggatt gtggagcaaa ctcccaaact tcccatggat
T A N S F L N Y R I V E Q T P K L P M D

FIG.2A

1261 ggactcttcc taatccaaac ctatgctgga atgttacagt tagctaaaca gtccttgaag
G L F L I Q T Y A G M L Q L A K Q S L K
1321 aagcaagata ctccctcagta caacttaacg atagagggtgt ctgacaaaaga tttcaagacc
K Q D T P Q Y N L T I E V S D K D F K T
1381 ctttgttttg tgcaaattcaa cgttattgtat atcaatgatc agatccccat ctttggaaaaaa
L C F V Q I N V I D I N D Q I P I F E K
1441 tcagattatg gaaacctgac tcttgctgaa gacacaaaca ttgggtccac catcttaacc
S D Y G N L T L A E D T N I G S T I L T
1501 atccaggcca ctgatgctga tgagccattt actgggagtt ctaaaaattct gtatcatatc
I Q A T D A D E P F T G S S K I L Y H I
1561 ataaaggagg acagtggagg acgcctgggg gttgacacag atccccatac caacaccgga
I K G D S E G R L G V D T D P H T N T G
1621 tatgtcataa ttaaaaagcc tcttgatttt gaaacagcag ctgtttccaa catttgttcc
Y V I I K K P L D F E T A A V S N I V F
1681 aaagcagaaa atcctgagcc tcttagtgttt ggtgtgaagt acaatgcaag ttctttgccc
K A E N P E P L V F G V K Y N A S S F A
1741 aagttcacgc ttattgtgac agatgtgaat gaagcacctc aattttccca acacgtattc
K F T L I V T D V N E A P Q F S Q H V F
1801 caagcgaaag tcagtggagg tcttagtata ggcactaaag tggcaatgt gactgccaag
Q A K V S E D V A I G T K V G N V T A K
1861 gatccagaag gtctggacat aagctattca ctgaggggag acacaagagg ttggcttaaa
D P E G L D I S Y S L R G D T R G W L K
1921 attgaccacg tgactgggtga gatcttagt gtggctccat tggacagaga agccggaagt
I D H V T G E I F S V A P L D R E A G S
1981 ccatatcggt tacaagtgggt ggccacagaa gtaggggggt cttccttaag ctctgtgtca
P Y R V Q V V A T E V G G S S L S S V S
2041 gagttccacc tgatccttat ggatgtgaat gacaaccctc ccaggctagc caaggactac
E F H L I L M D V N D N P P R L A K D Y
2101 acgggcttgt tcttctgcca tcccctcagt gcacctggaa gtctcatttt cgaggctact
T G L F F C H P L S A P G S L I F E A T
2161 gatgatgatc agcacttatt tcggggtccc cattttacat tttccctcgg cagtggaagc
D D D Q H L F R G P H F T F S L G S G S
2221 ttacaaaacg actgggaagt ttccaaaatc aatggtaatc atgcccgaact gtctaccagg
L Q N D W E V S K I N G T H A R L S T R
2281 cacacagact ttgaggagag ggcgtatgtc gtcttgatcc gcatcaatga tgggggtcgg
H T D F E E R A Y V V L I R I N D G G R
2341 ccacccttgg aaggcattgt ttcttacca gttacattct gcagttgtgt ggaaggaagt
P P L E G I V S L P V T F C S C V E G S
2401 tgtttccggc cagcaggta ccagactggg atacccactg tgggcatggc agttggata
C F R P A G H Q T G I P T V G M A V G I

FIG.2B

2461 ctgctgacca cccttctgg tattggata atttagcag ttgtgtttat ccgcataaaag
L L T T L L V I G I I L A V V F I R I K
2521 aaggataaaag gcaaagataa tggtgaaaagt gctcaagcat ctgaagtcaa acctctgaga
K D K G K D N V E S A Q A S E V K P L R
2581 agctgaattt gaaaaggaat gtttgeattt atatagcaag tgctatttca gcaacaacca
S

2641 tctcatccta ttactttca tctaacctgc attataattt tttaaacaga tattccctct
2701 tgtccttaa tatttgctaa atattcttt tttgaggtgg agtcttgctc tgtcgcccag
2761 gctggagtagc agtgggtgtga tcccaagctca ctgcaacctc cgccctctgg gttcacatga
2821 ttctcctgcc tcagcttcct aagtagctgg gtttacaggc acccaccacc atgcccagct
2881 aatttttgta ttttaatag agacggggtt tcgcccattt gccaggatgg tcttgeactc
2941 ctgacgtcaa gtgatctgcc tgccttggtc tcccaataca ggcataacc actgcaccca
3001 cctacttaga tatttcatgt gctatagaca ttagagagat ttttcatttt tccatgacat
3061 ttttcctctc tgcaaatttgc tttagctactt gtgttttcc cttttggggc aagacagact
3121 cattaaatat tctgtacatt ttttctttat caaggagata tatcagtgtt gtctcataga
3181 actgcctgga ttccatttat gtttttctg attccatcct gtgtcccctt catccttgac
3241 tcctttggta tttcaactgaa ttcaaacat ttgtcagaga agaaaaaaagt gaggactcag
3301 gaaaaataaa taaataaaag aacagcctt tgcggcccg aattc

FIG.2C

20	40	60
MARKKFSGLEISLIVLFVIV	TIIAIALIVVLATKTPAVDE	ISDSTSTPATTRVTNTNPSDS
80	100	120
GKCPNVLNDPVNVRINCIPE	QFPTEGICAQRGCCWRPWND	SLIPWCFFVDNHGYNVQDMT
140	160	180
TTSIGVEAKLNRIPSPLFG	NDINSVLFTTQNQTPNRFRF	KITDPNNRRYEVPHQYVKEF
200	220	240
TGPTVSDTLYDVKVAQNPFS	IQVIRKSNKGKLFDTSIGPL	VYSDOYLOQISARLPSDYIYG
260	280	300
IGEQVHKRFRHDLWSKTWPI	FTRDQLPGDNNNNLYGHQTF	FMCIEDTSGKSFGVFLMNSN
320	340	360
AMEIFIQPTPIVTYRVTGGI	LDFYILLGDTPEQVVQQYQQ	LVGLPAMPAYNLGFQLSRW
380	400	420
NYKSLDVVKEVVRNREAGI	PFDTQVTDIDYMEDKKDFTY	DQVAFNGLPQFVQDLHDHGQ
440	460	480
KYVIILDPAISIGRRANGTT	YATYERGNTQHVVWINESDGS	TPIIGEVWPGLTVYPDFTNP
500	520	540
NCIDWWANECSIFHQEVQYD	GLWIDMNEVSSFIQGSTKGC	NVNKLNYPPFTPDIILDKLMLY
560	580	600
SKTICMDAVQNWGKQYDVHS	LYGYSMAIATEQAVQKVFPN	KRSFILTRSTFAGSGRHAH
620	640	660
WLGDNTASWEQMEWSITGML	EFSLFGIPLVGADICGFVAE	TTEELCRRWMQLGAFYPFSR
680	700	720
NHNSDGYEHQDPAFFGQNSL	LVKSSRQYLTIRYTLLPFLY	TLFYKAHVGETVARPVLHE
740	760	780
FYEDTNSWIEDTEFLWGPAL	LITPVLKQGADTVSAYIPDA	IWYDYESGAKRPWRKQRVDM
800	820	840
YLPADKIGLHLRGGYIPIQ	EPDVTTTASRKKNPLGLIVAL	GENNTAKGDFFWDDGETKDT
860	880	900
IQNGNYILYTFVSNNLDI	VCTHSSYQEGTTLAFQTVKI	LGLTDSVTEVRVAENNQPMN
920	940	960
AHSNFTYDASNQVLLIADLK	LNLGRNFSVQWNQIFSNER	FNCYPDADLATEQKCTQRGC
980	1000	1020
VWRTGSSLSKAPECYFPRQD	NSYSVNSARYSSMGITADLQ	LNTANARIKLPSPDPISTLRV
1040	1060	1080
EVKYHKNDMLQFKIYDPQKK	RYEVPVPLNIPTTPISTYED	RLYDVEIKENPFGIQIRRHS
1100	1120	1140
SGRVIWDSWLPGFAFDQFI	QISTRLPSEYIYGFGEVEHT	AFKRDLNWNTWGMFRDQPP
1160	1180	1200
GYKLNSYGFHPYYMALEEEG	NAHGVFLLNSNAMDVTFOPT	PALTYRTVGGILDYMFGLGP
1220	1240	1260
TPQVATKQYHEVIGHPVMPA	YWALGFQLCRYGYANTSEVR	ELYDAMVAANIPYDVQYTDI

FIG.3A

1280	1300	1320
DYMERQLDFTIGEAFQDLPQ	FVDKIRGEGMRYIIILDPAI	SGNETKTPAFAERGQQNDVF
1340	1360	1380
VWPNTNDICWAKVWPDLPN	ITIDKTLTEDEAVNASRAHV	AFPDFFRTSTAEWWAREIVD
1400	1420	1440
FYNEKMKFDGLWIDMNEPSS	FVNGTTTNQCRNDELNYPPY	FPELTKRTDGLHFRTICMEA
1460	1480	1500
EQILSDGTSVLHYDVHNLYG	WSQMKPTHDALQKTTGKRG	VISRSTYPTSGRWGGHWLG
1520	1540	1560
NYARWDNMDKSIIGMMEFSL	FGISYTGADICGFFNNSEYH	LCTRWMQLGAFYPYSRNHN
1580	1600	1620
ANTRRQDPASWNETFAEMSR	NILNIRYTLLPYFYTQMHEI	HANGTVIRPLLHEFFDEKP
1640	1660	1680
TWDIFKQFLWGPAPMVTPL	EPYVQTVNAYVPNARWFDYH	TGKDIGHVRGQFQTFNASYDT
1700	1720	1740
INLHVRRGGHILPCQEPAQNT	FYSRQKHMKLIVAADDNQMA	QGSLFWDDGESIDTYERDLY
1760	1780	1800
LSVQFNLNQTTLTSTILKRG	YINKSETRLGSLHWWGKGTT	PVNAVTLTYNGNKNSLPFNE
1820	1827	
DTTNMILRIDLTTHNVTLLEE	PIEINWS	

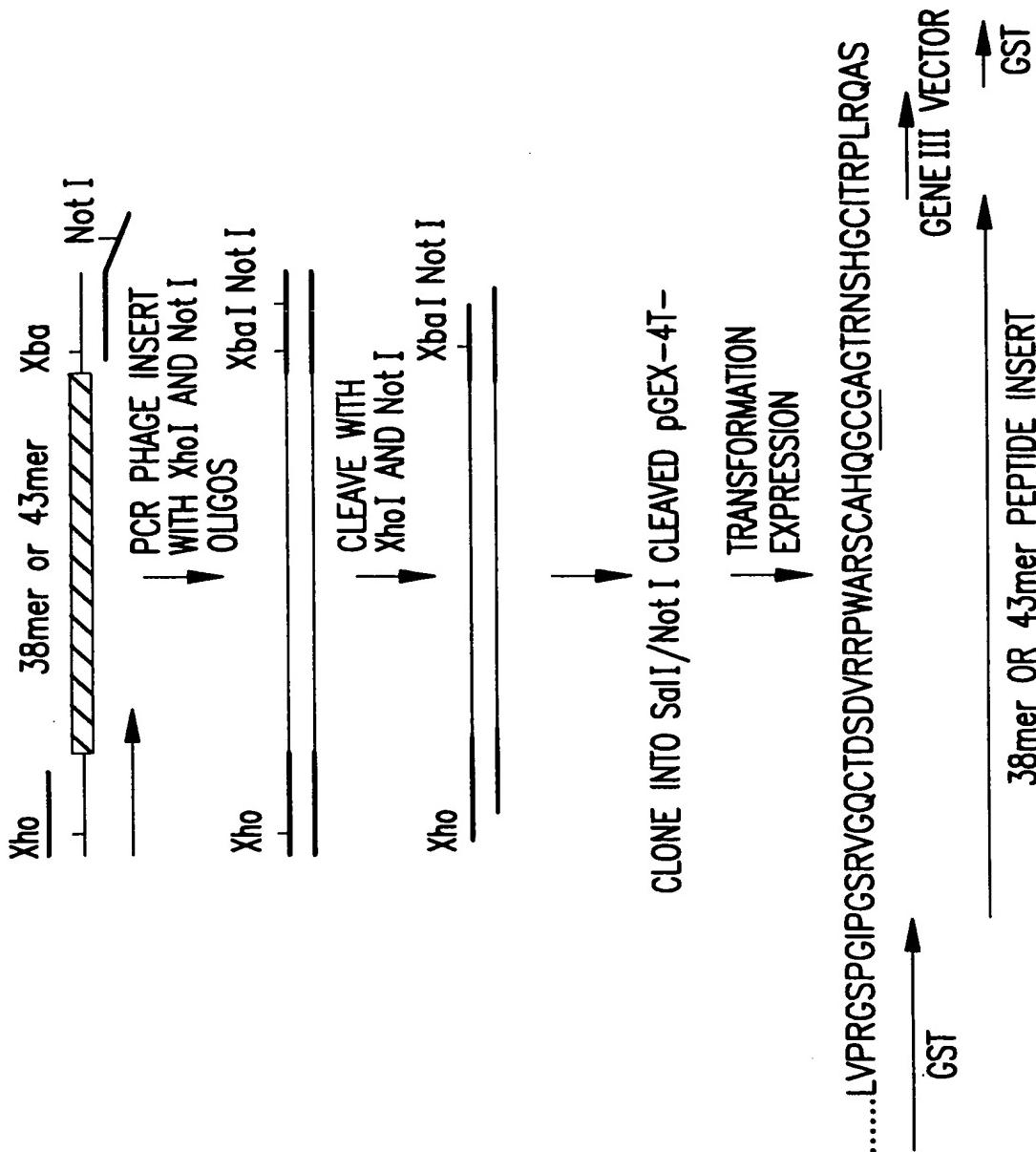
FIG.3B

1 gccttactgc aggaaggcac tccgaagaca taagtcggtg agacatggct gaagataaaa
M A E D K
61 gcaagagaga ctccatcgag atgagtatga agggatgcc aacaaacaac gggtttgtcc
S K R D S I E M S M K G C Q T N N G F V
121 ataatgaaga cattctggag cagaccccg atccaggcag ctcaacagac aacctaagc
H N E D I L E Q T P D P G S S T D N L K
181 acagcaccag gggcatcctt ggctcccagg agcccgactt caagggcgtc cagccctatg
H S T R G I L G S Q E P D F K G V Q P Y
241 cggggatgcc caaggaggtg ctgttccagt tctctggca gggccgctac cgcatacctc
A G M P K E V L F Q F S G Q A R Y R I P
301 gggagatcct cttctggctc acagtggctt ctgtgctggt gctcatcgcg gccaccatag
R E I L F W L T V A S V L V L I A A T I
361 ccatcattgc cctctctcca aagtgcctag actgggtggca ggaggggccc atgtaccaga
A I I A L S P K C L D W W Q E G P M Y Q
421 tctacccaag gtcttcaag gacagtaaca aggatggaa cgagatctg aaaggtattc
I Y P R S F K D S N K D G N G D L K G I
481 aagataaaact ggactacatc acagcttaa atataaaaac tgtttggatt acttcatttt
Q D K L D Y I T A L N I K T V W I T S F
541 ataaatcgtc cctaaagat ttcatatg gtgtgaaga tttccggaa gttgatccca
Y K S S L K D F R Y G V E D F R E V D P
601 ttttggAAC gatggaaagat tttgagaatc tggtgcagc catacatgat aaaggtttaa
I F G T M E D F E N L V A A I H D K G L
661 aattaatcat cgatttcata ccaaaccaca cgagtataa acatatttg tttcaattga
K L I I D F I P N H T S D K H I W F Q L
721 gtcggacacg gacaggaaaa tatactgatt attatatctg gcatgactgt acccatgaaa
S R T R T G K Y T D Y Y I W H D C T H E
781 atggcaaaac cattccaccc aacaactggt taagtgtgt tgaaaactcc agttggcact
N G K T I P P N N W L S V Y G N S S W H
841 ttgacgaagt gcaaaccAA tgttatTTTc atcagtttat gaaagagcaa cctgattttaa
F D E V R N Q C Y F H Q F M K E Q P D L
901 attccgcaa tcctgatgtt caagaagaaa taaaagaaaat ttacggttc tggctcacaa
N F R N P D V Q E E I K E I L R F W L T
961 agggtgttga tggtttagt ttggatgctg ttaaattcct cctagaagca aagcacctga
K G V D G F S L D A V K F L L E A K H L

FIG.4A

1021 gagatgagat ccaagtaaat aagacccaaa tcccggacac ggtcacacaa tactcgagc
R D E I Q V N K T Q I P D T V T Q Y S E
1081 tgtaccatga cttcaccacc acgcaggctgg gaatgcacga cattgtccgc agcttccggc
L Y H D F T T T Q V G M H D I V R S F R
1141 agaccatgga ccaatacagc acggagcccg gcagatacag gttcatgggg actgaagcct
Q T M D Q Y S T E P G R Y R F M G T E A
1201 atgcagagag tattgacagg accgtgatgt actatggatt gccatttatc caagaagctg
Y A E S I D R T V M Y Y G L P F I Q E A
1261 attttccatt caacaattac ctacatgc tagacactgt ttctggAAC agcgtgtatg
D F P F N N Y L S M L D T V S G N S V Y
1321 aggttattcac atcctggatg gaaaacatgc cagaaggaaa atggcctaAC tggatgattg
E V I T S W M E N M P E G K W P N W M I
1381 gtggaccaga cagttcacgg ctgacttcgc gtttggggaa tcagtatgtc aacgtgtatga
G G P D S S R L T S R L G N Q Y V N V M
1441 acatgcttct tttcacactc cctggAACTC ctataactta ctatggagaa gaaattggaa
N M L L F T L P G T P I T Y Y G E E I G
1501 tggaaatat tgttagccgca aatctcaatg aaagctatga tattastacc cttcgctcaa
M G N I V A A N L N E S Y D I N T L R S
1561 agtcaccaat gcagtggac aatagttcaa atgctggTTT ttctgaagct agtaacacct
K S P M Q W D N S S N A G F S E A S N T
1621 ggttacctac caattcagat taccacactg tgaatgttga tgtccaaaAG actcagccca
W L P T N S D Y H T V N V D V Q K T Q P
1681 gatcggtttt gaagttatat caagattaa gtctacttca tgccaatgag ctactcctca
R S A L K L Y Q D L S L L H A N E L L L
1741 acagggcgtg gtttgccat ttgaggaatg acagccacta tggatgtac acaagagagc
N R G W F C H L R N D S H Y V V Y T R E
1801 tggatggcat cgacagaatc ttatcggtgg ttctgaattt tggagaatca acactgttaa
L D G I D R I F I V V L N F G E S T L L
1861 atctacataa tatgatttcg ggccttcccg ctaaaataag aataaggta agtaccaatt
N L H N M I S G L P A K I R I R L S T N
1921 ctgccacaa aggcaataaa gttgatcacaa gtggcatttt tctggacaag ggagagggac
S A D K G S K V D T S G I F L D K G E G
1981 tcatcttga acacaacacg aagaatctcc ttcatcgcca aacagcttc agagatagat
L I F E H N T K N L L H R Q T A F R D R
2041 gctttgttcc caatcgagca tgctattcca gtgtactgaa catactgtat acctcggtt
C F V S N R A C Y S S V L N I L Y T S C
2101 aggcaccttt atgaagagat gaagacactg gcatttcagt gggattgtaa gcatttgtaa
2161 tagcttcatg tacagcatgc tgcttggtga acaatcatta attcttcgtat atttctgttag
2221 cttgaatgta accgctttaa gaaaggttct caaatgtttt gaaaaaaaata aaatgtttaa
2281 aagt

EXPRESSION OF PHAGE INSERTS AS GST FUSION

**FIG. 5A**

1. CLASS
DRAFT

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P31	1	10	20	30	Clone #
	SARDSGPAEDGSRAVRLNGVENANTRKSSRSNPRGRRHP				
	SARDSGPAEDGSRAVRLNG				101
	DGSRAVRLNGVENANTRKSSR				102
	ENANTRKSSRSNPRGRRHP				103
	TRKSSRSNPRG				119
Pax2	1	10	20	30	Clone #
	STPPSREAYSRPYSVDSDDSDTNAKHSSHNRRLRTRSRPN				
	STPPSREAYSRPYSVDSDDSD				104
	SRPYSVDSDDSDTNAKHSSHNR				105
	TNAKHSSHNRRLRTRSRPN				106
DCX8	1	10	20	30	Clone #
	RYKHDIGCDAGVDKSSSVRGCGAHSSPPRAGRGPRTMVSRL				
	RYKHDIGCDAGVDKSSSVRGCG				107
	GCDAGVDKSSSVRGCGAHSSPPRA				108
	GAHSSPPRAGRGPRTMVSRL				109

FIG.5B

DRAFTS

P31	1	10	20	30	Clone #
	SARDSGPAEDGSRAVRLNGVEN <u>A</u> NTRKSSRSNPRGRRHP				
		EN <u>A</u> NTRKSSRSNPRGRRHP			103
		EN <u>A</u> NTRKSSR			110
			TRKSSRSNPRG		119
			RKSSRSNPRG		111
			SNPRGRRHP		112
Pax2	1	10	20	30	Clone #
	STPPSREAYSRPYSVDS	SD	DTNA <u>A</u> KHSSHNRRLRTRSRPN		
			TNA <u>A</u> KHSSHNRRLRTRSRPN		106
			TNA <u>A</u> KHSSHN		113
			SSHNRRLRTR		114
			RRLRTRSRPN		115
SN10	1	10	20	30	Clone#
	RVGQCTDSDVRRPWARSCAH <u>Q</u> GCGAGTRNSHGCI	TRPLRQASAH			
	RVGQCTDSDVRRPWARSCA				116
	VRRPWARSCAH <u>Q</u> GCGAGTRNS				117
		GTRNSHGCI	TRPLRQASAH		118

FIG.5C

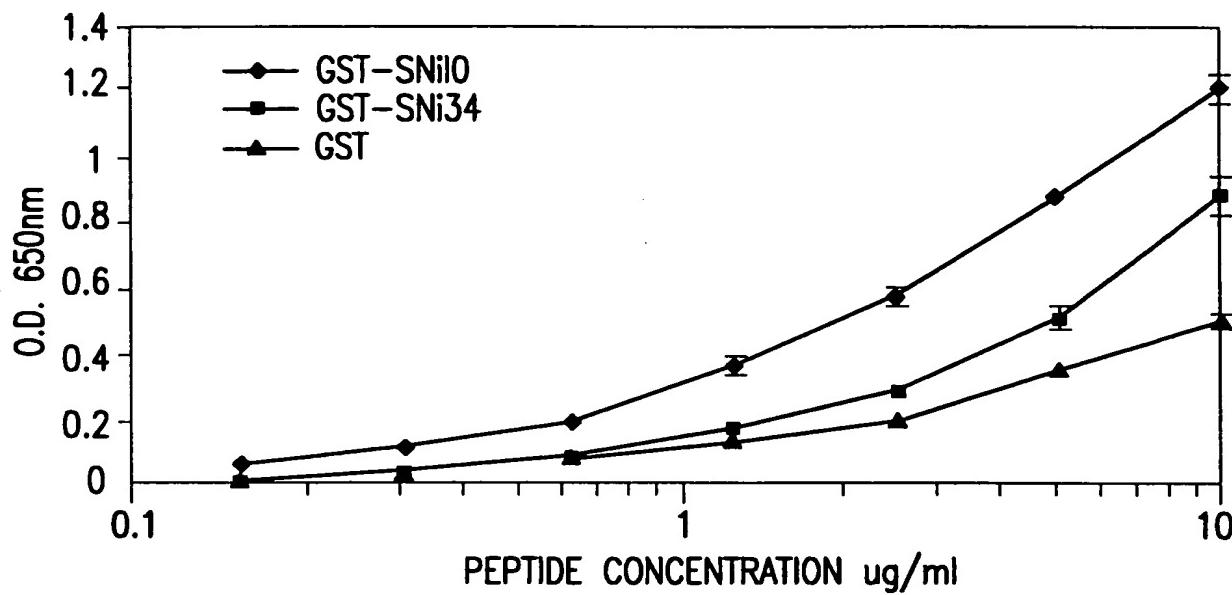


FIG.6A

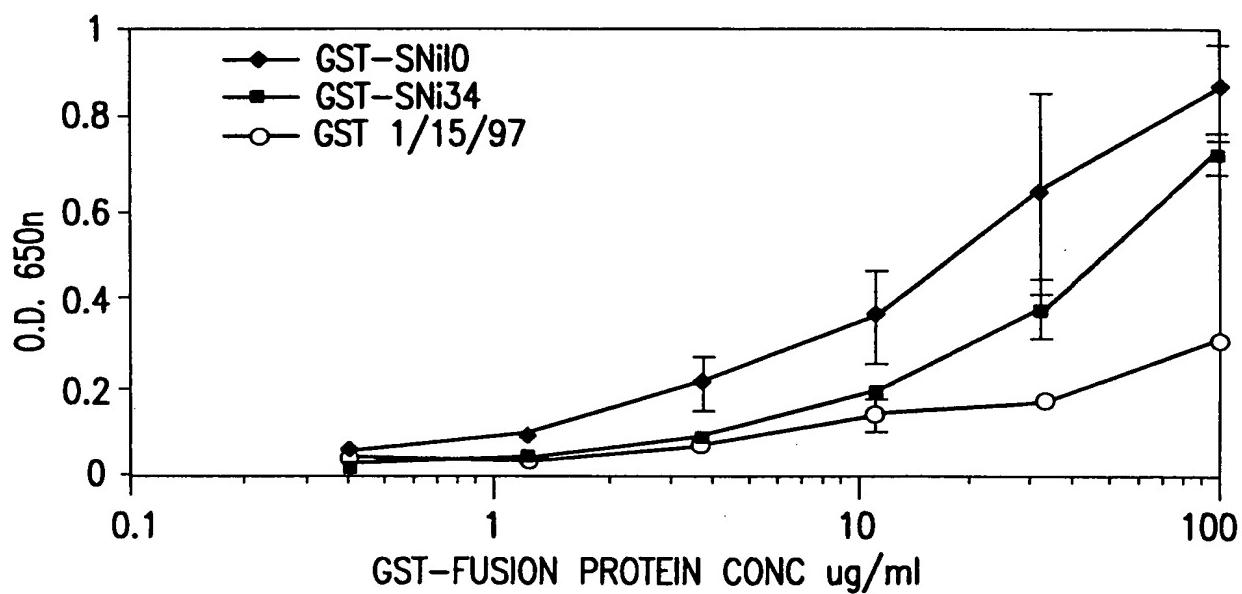


FIG.6B

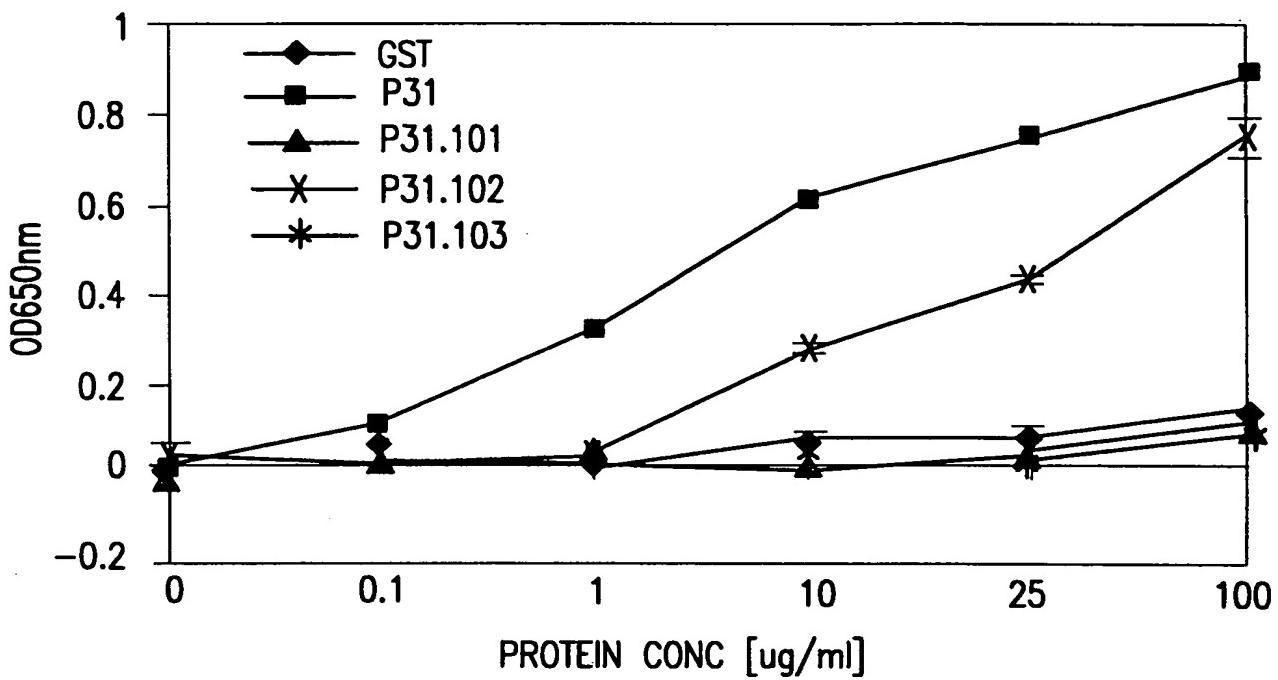


FIG. 7A

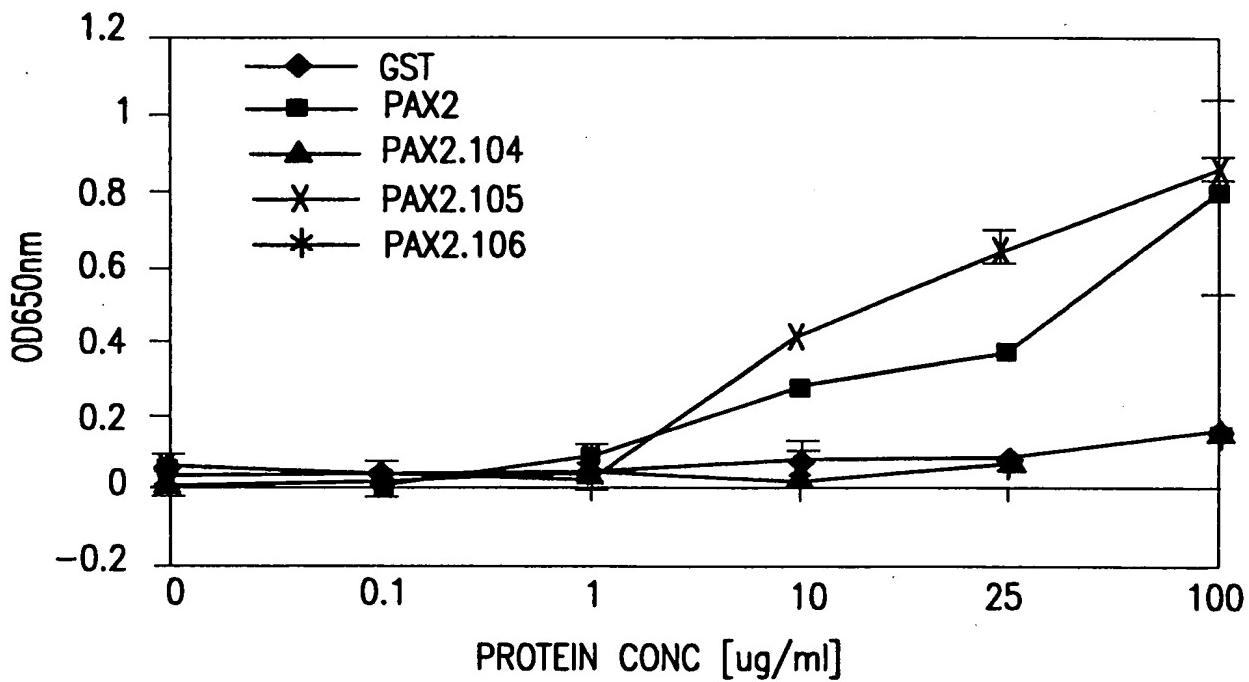


FIG. 7B

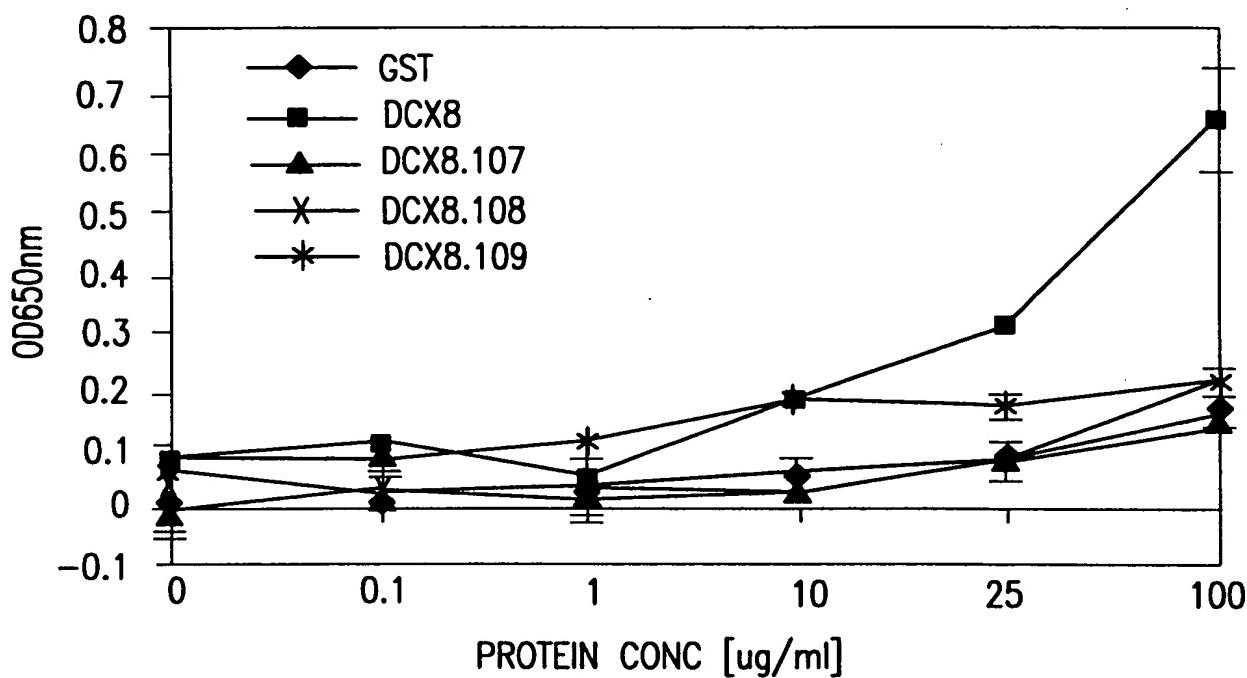


FIG. 7C

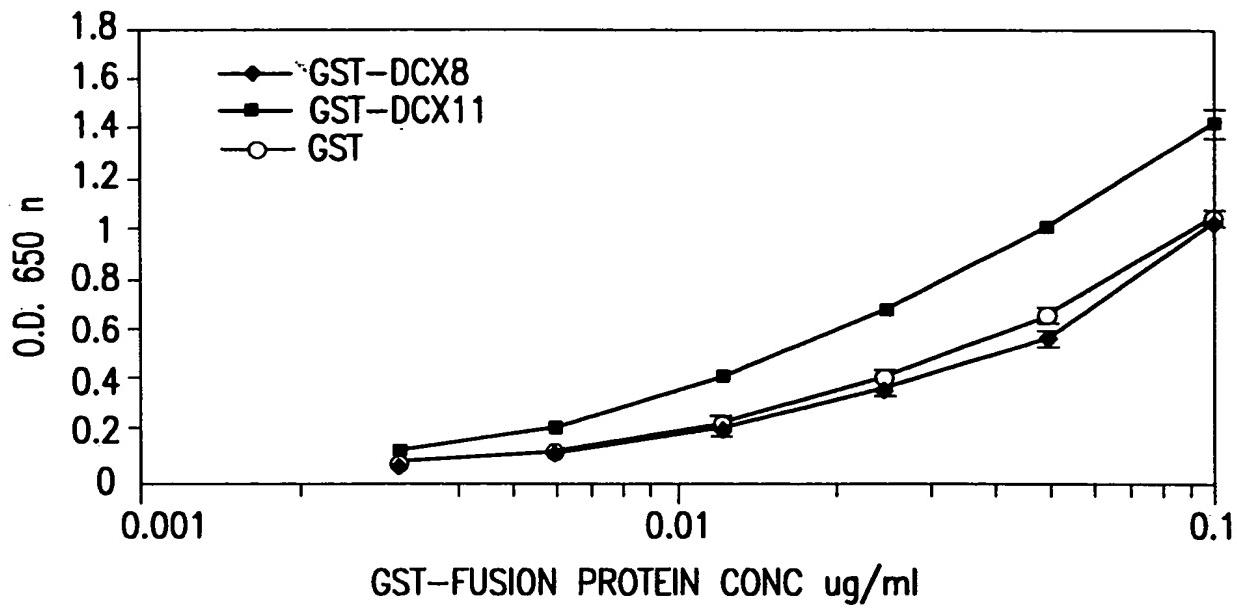


FIG.7D

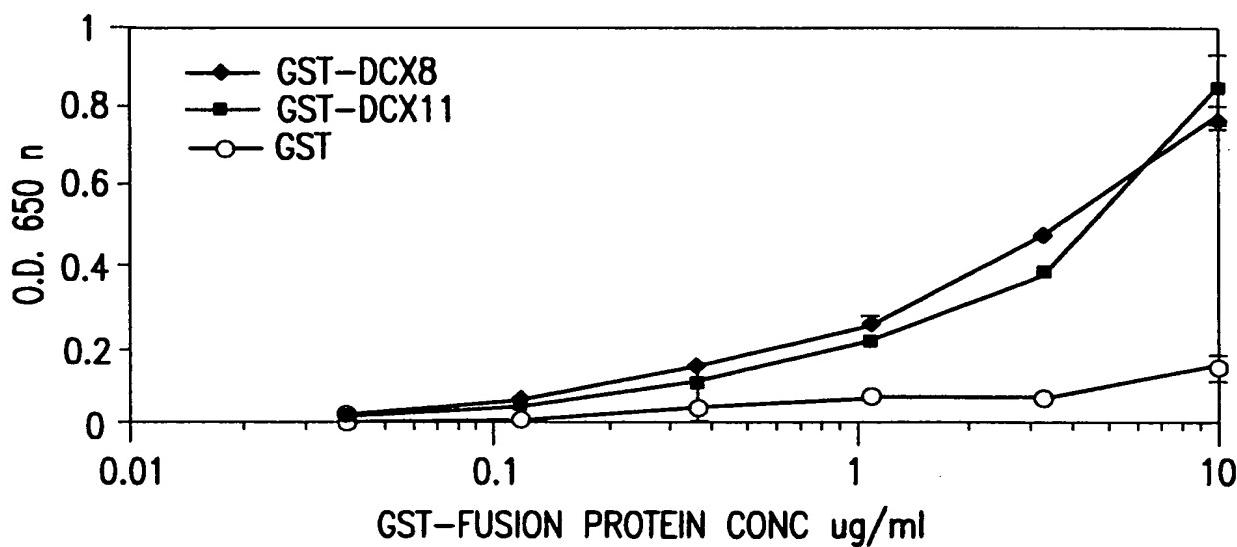


FIG.7E

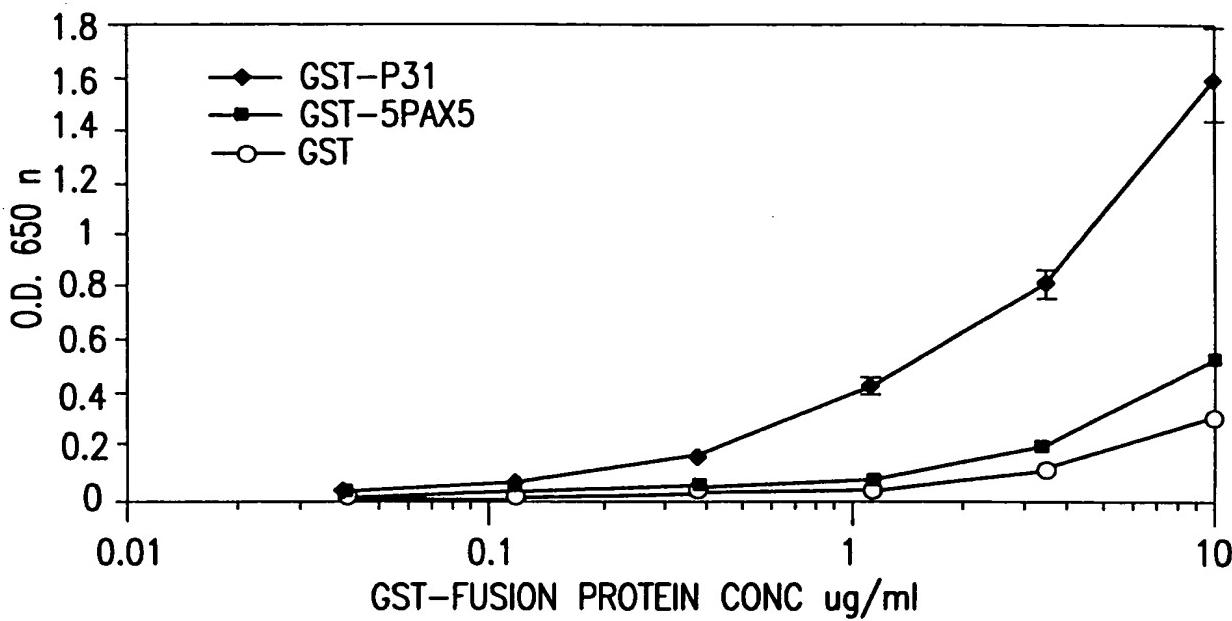


FIG.7F

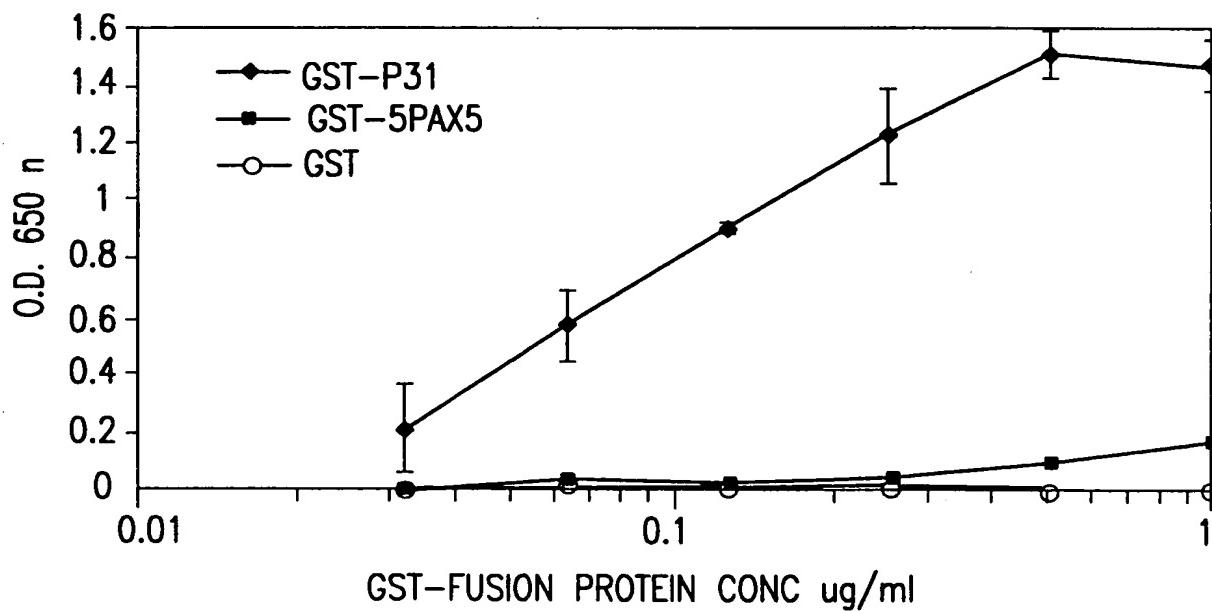


FIG.7G

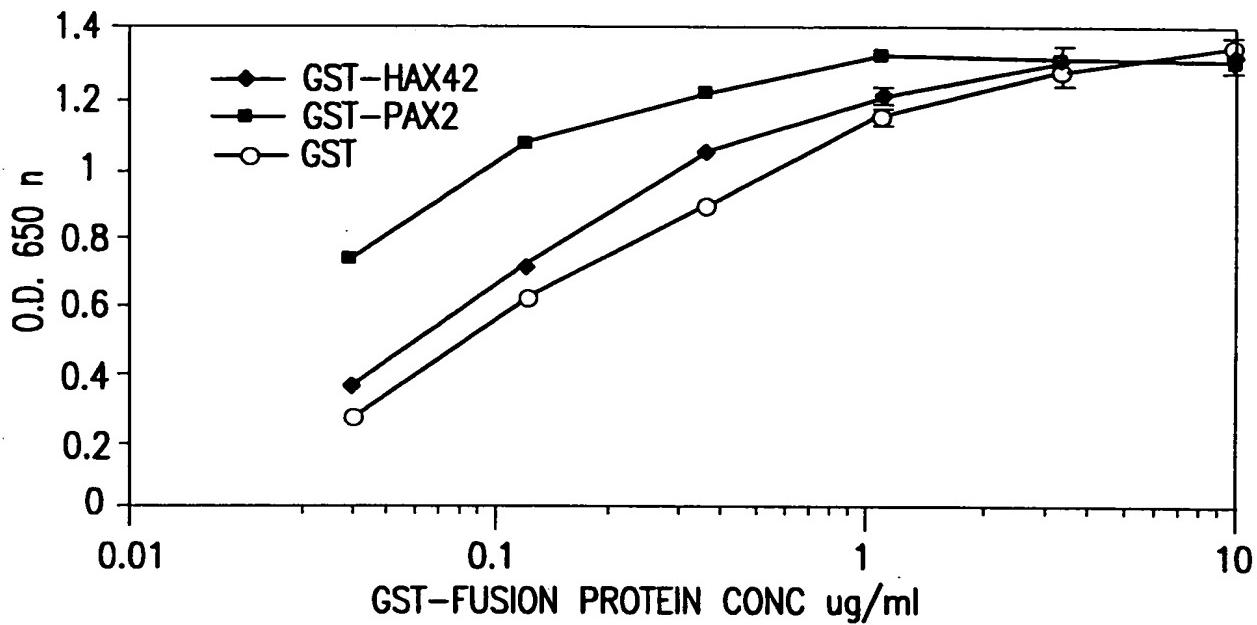


FIG.7H

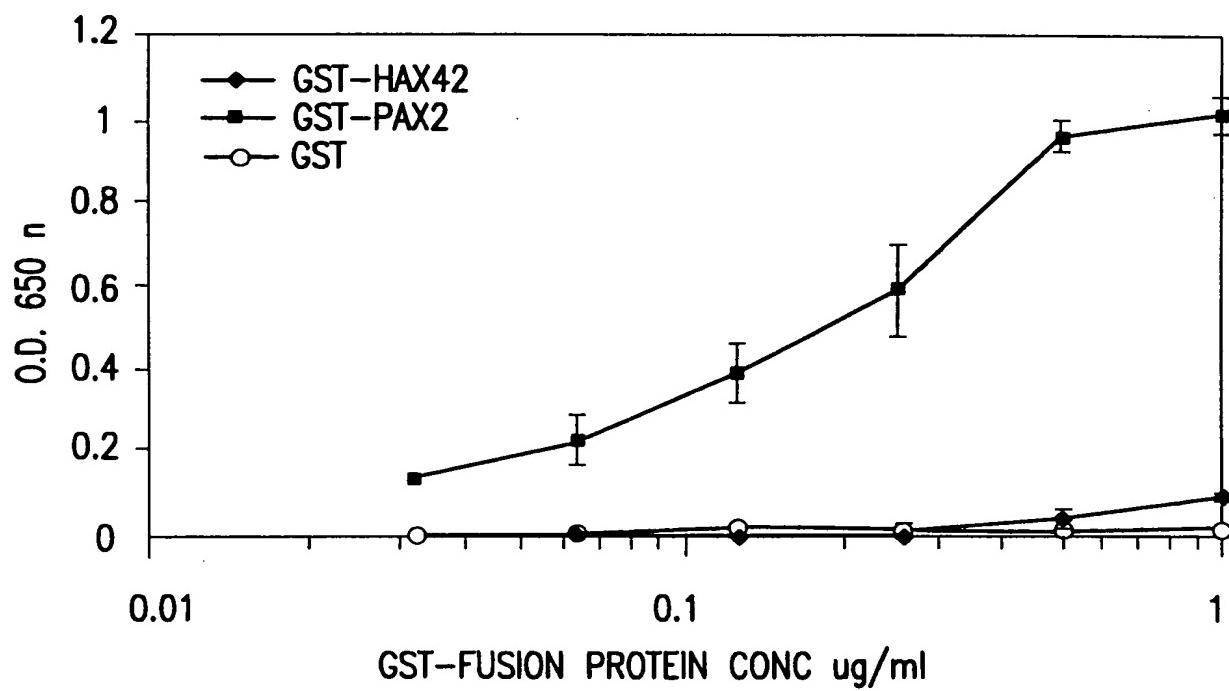


FIG.7I

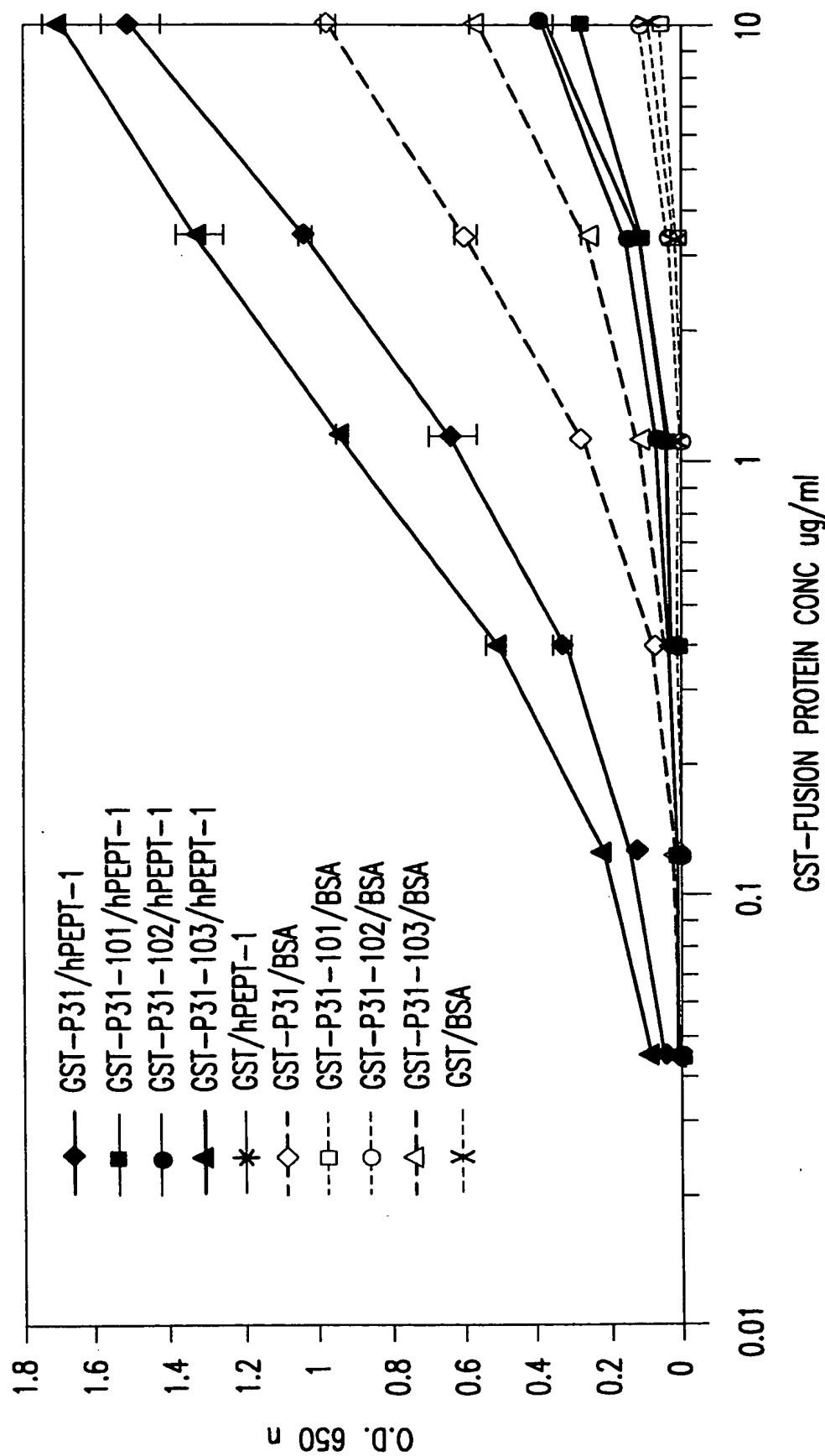


FIG. 7J

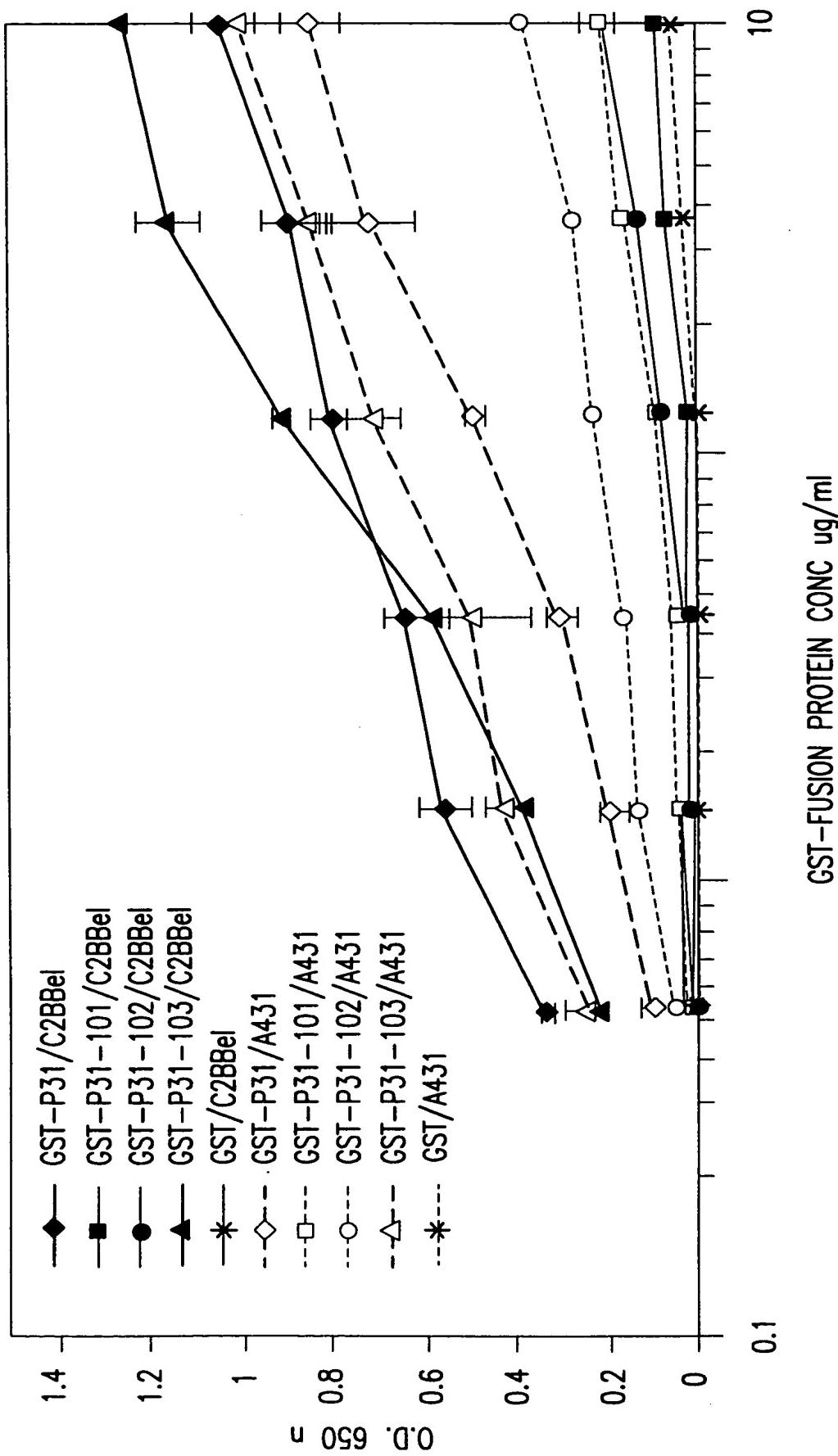


FIG. 7K

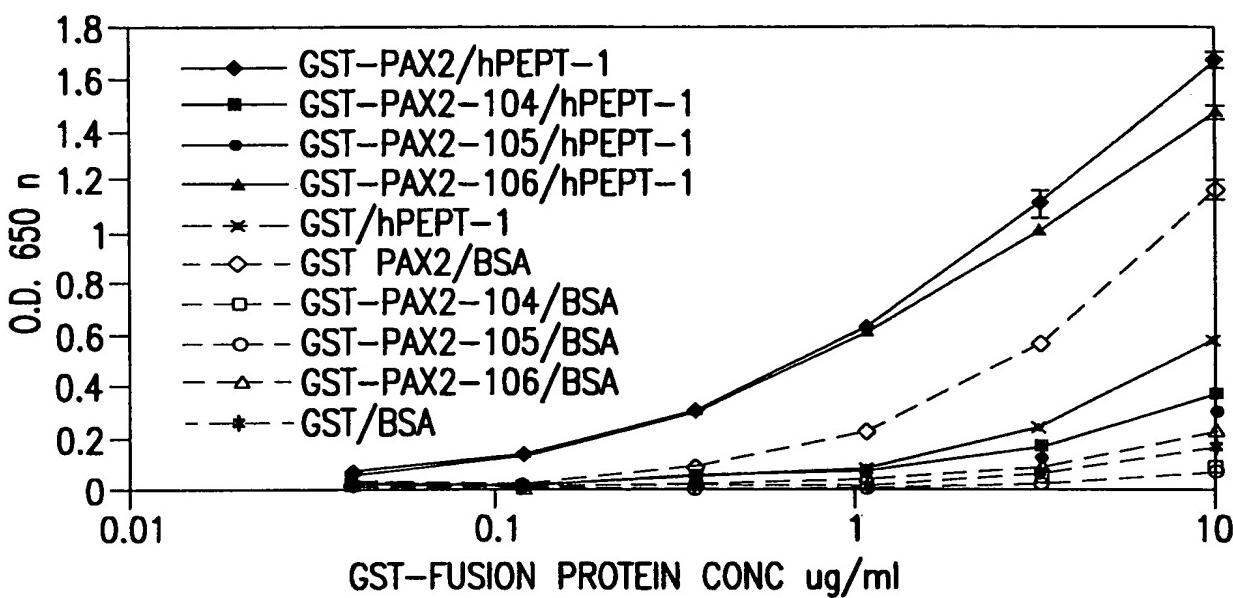


FIG. 7L

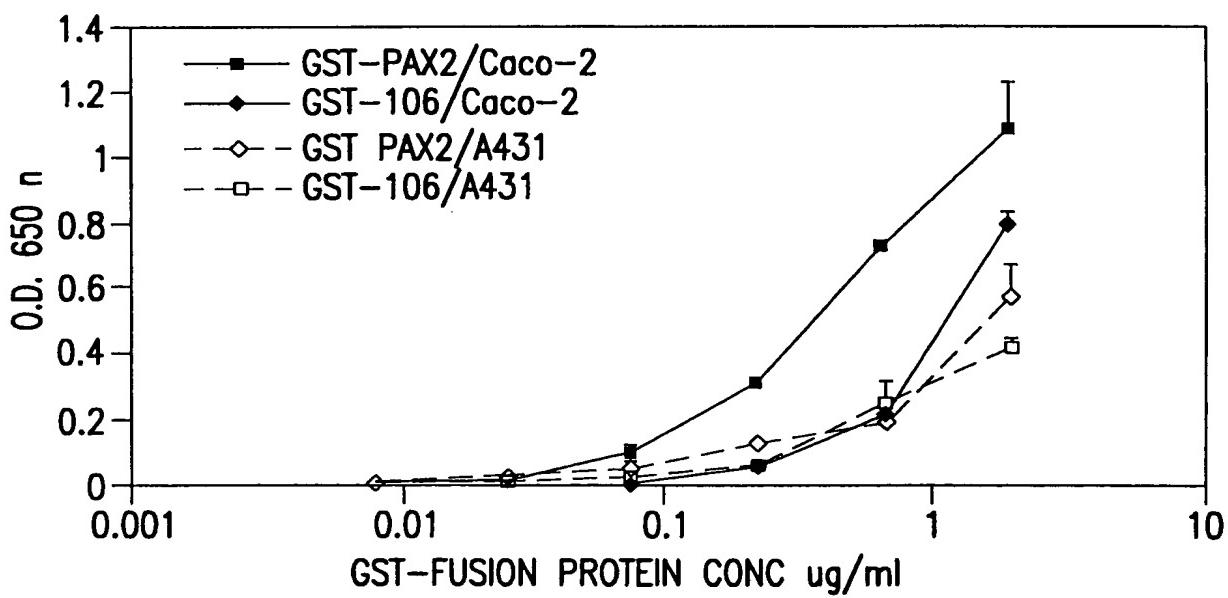


FIG. 7M

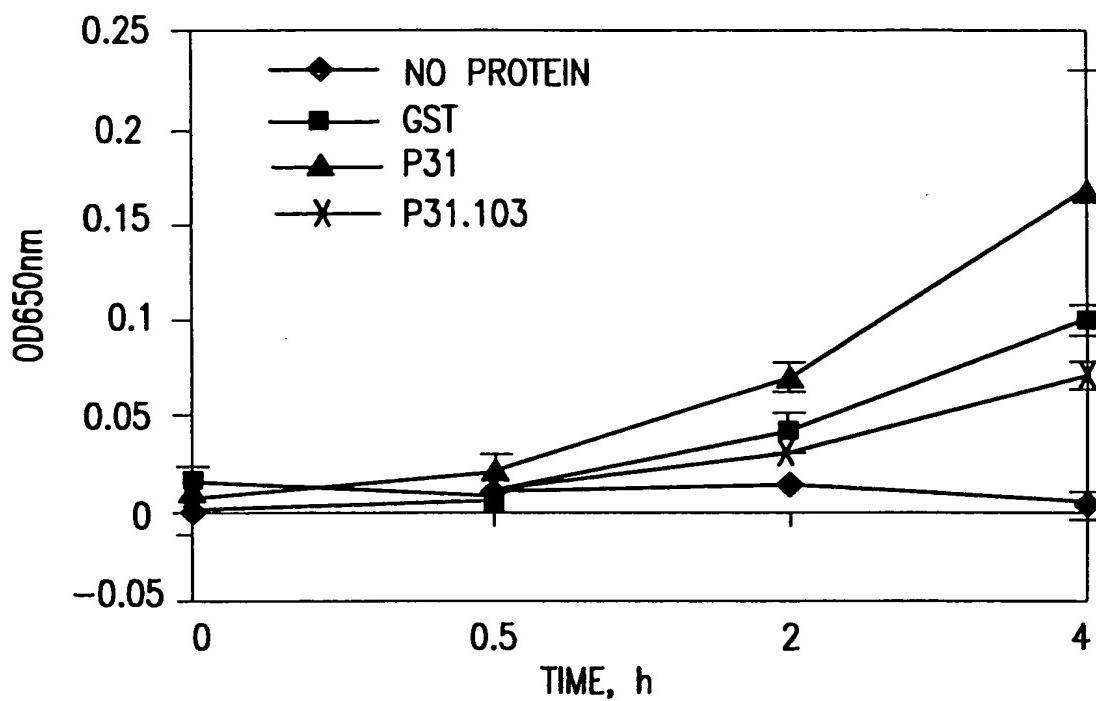


FIG.8A

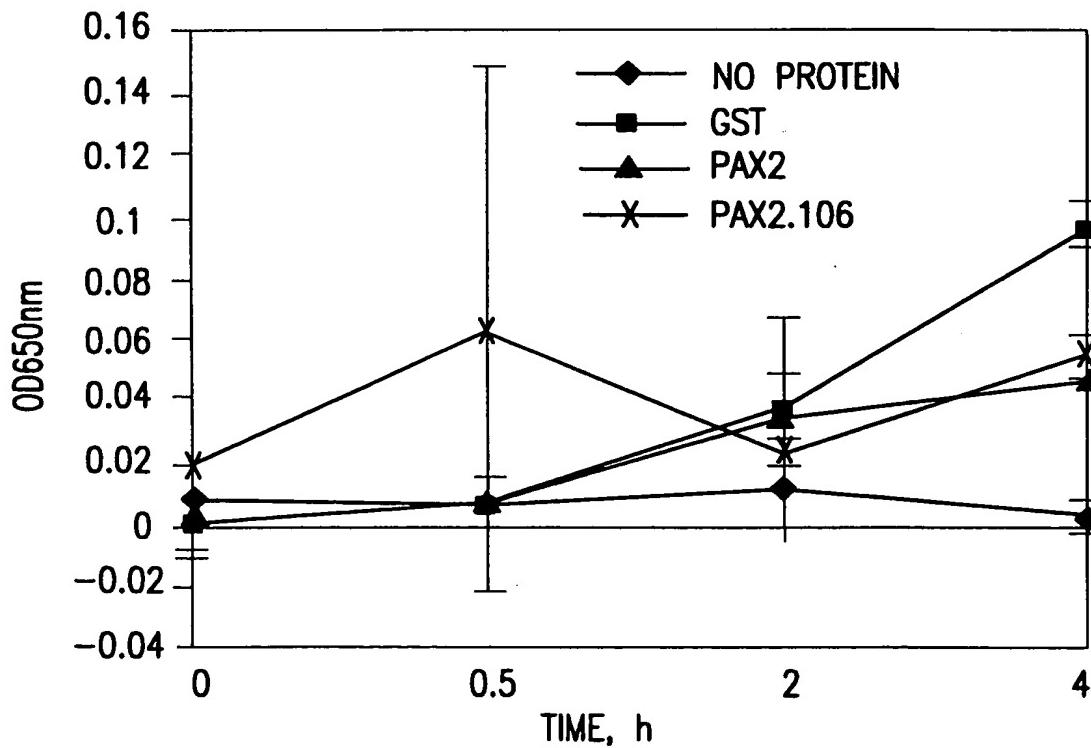


FIG.8B

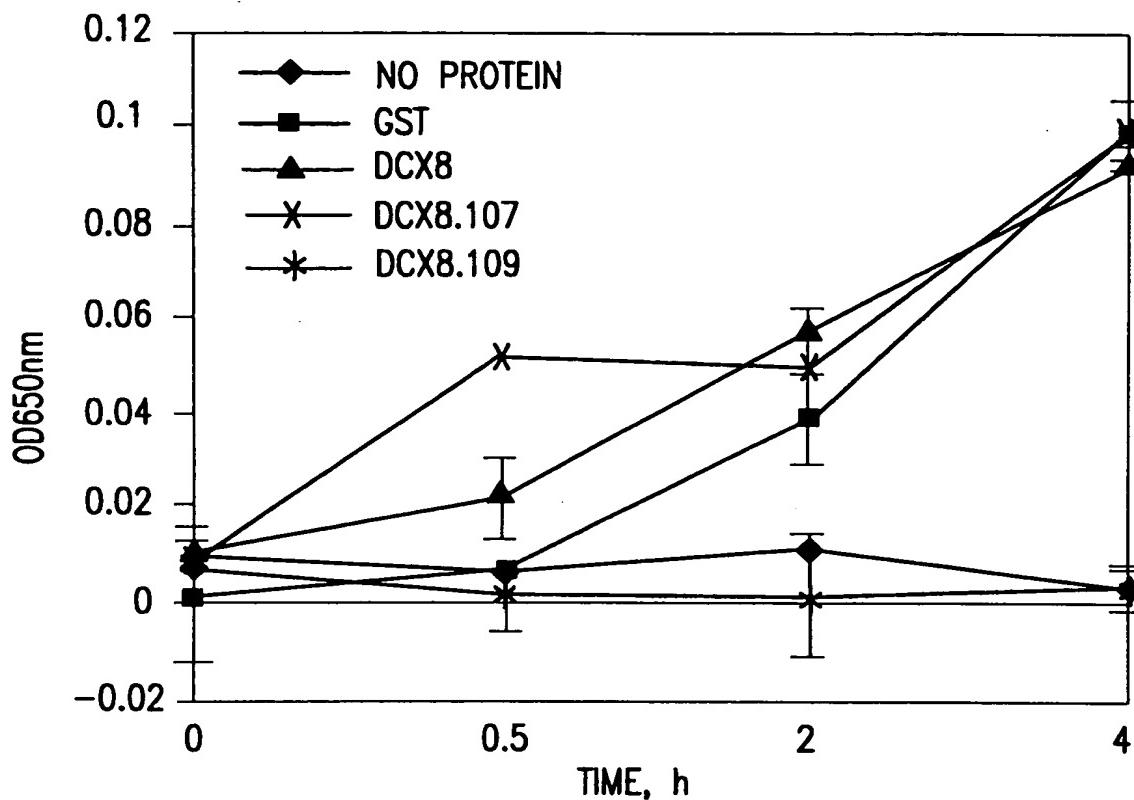


FIG.8C

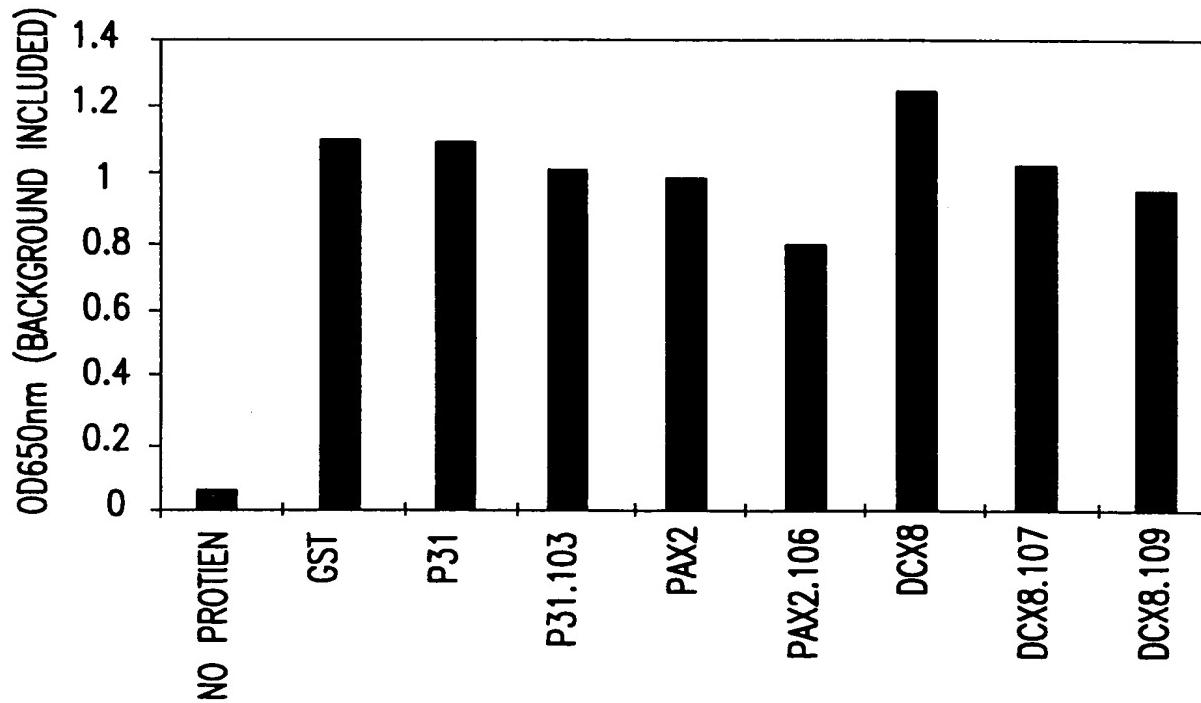


FIG.8D

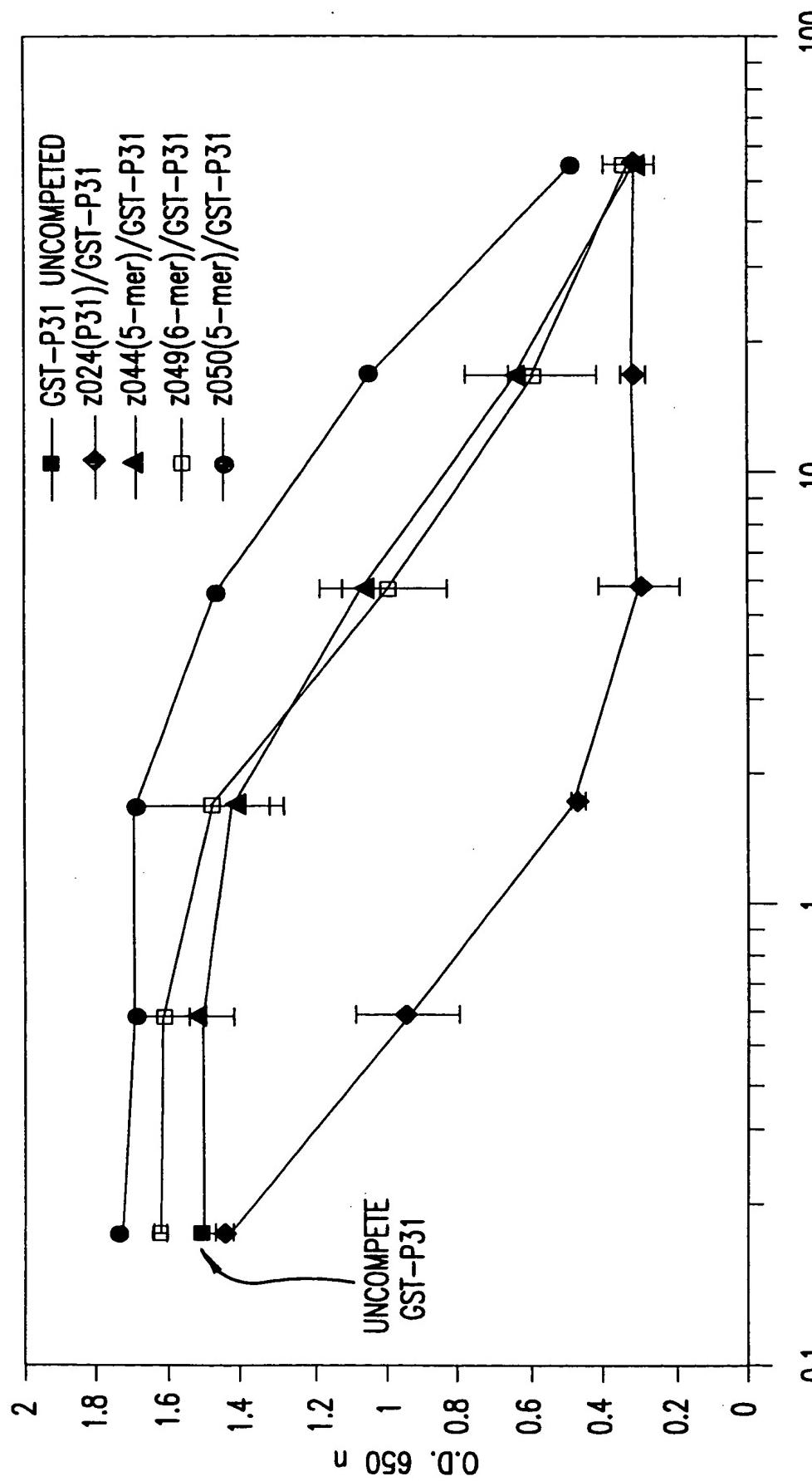


FIG. 9A

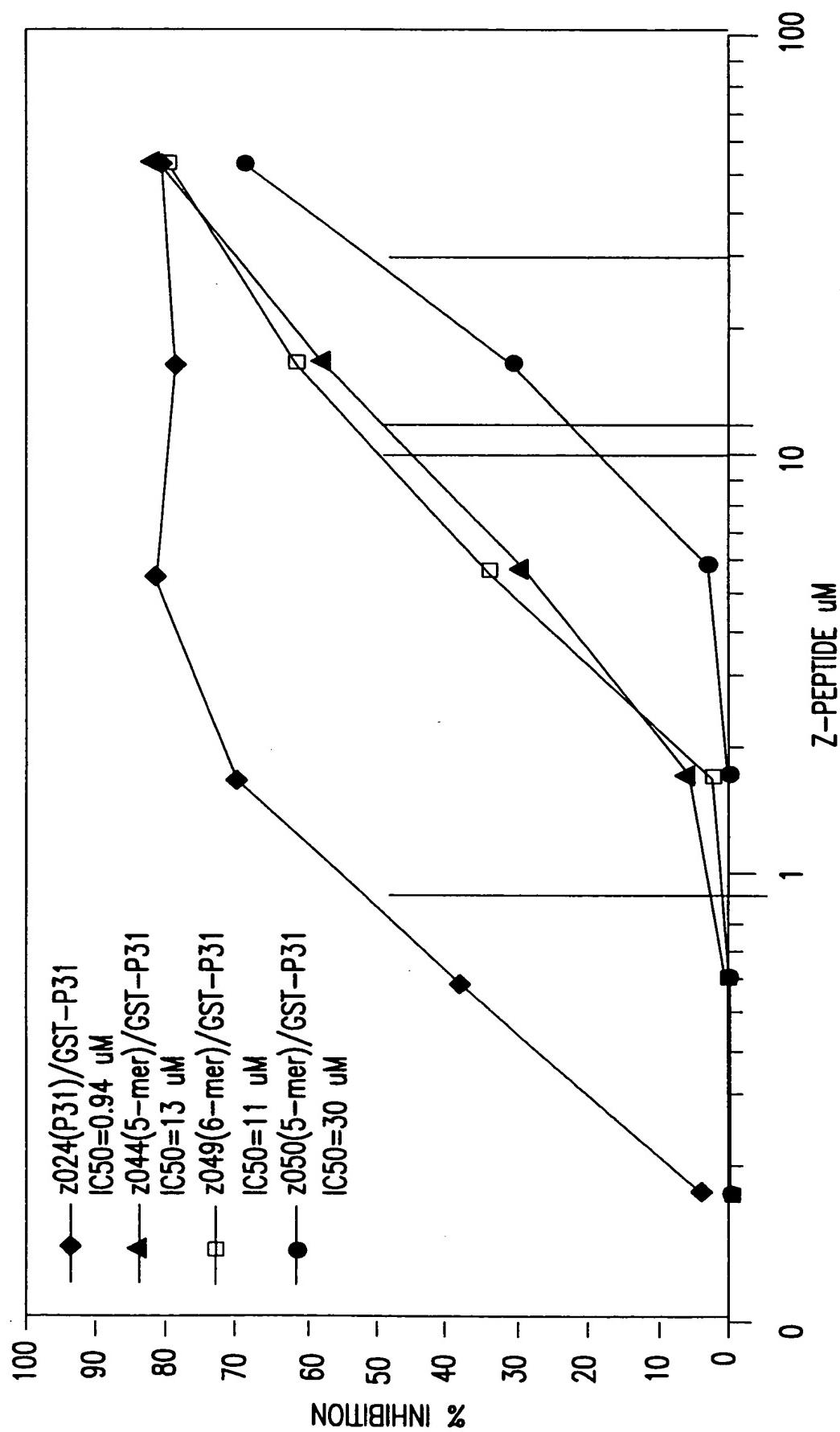


FIG. 9B

<u>Peptide Name</u>	<u>Sequence</u>	<u>pI</u>	<u>IC₅₀</u>	<u>GST/C2BBe1</u>
ELAN024 (P31)	SARDSGPAEDGSRRAVRLNGVENANTRKSSRSNPRGRRRHPG	11.88	0.5-2.2	+++
101	SARDSGPAEDGSRRAVRLNG			
102	DGSRAVRLNGVENANTRKSSR			
103	ENANTRKSSRSNPRGRRRHPG			
110	ENANTRKSSR			
111	RKSSRSNPRG			
112	SNPRGRRRKP			
119	TRKSSRSNPRG			
728	ZENANTRKSSRSNPRGRRRHPG	12.28	0.5-1.7	
729	ZTRKSSRSNPRG	12.40	5.5-15	
730	ZENANTRKSSRSNPRG	11.81>50		
731	ZTRKSSRSNPRGRRRHPG	12.70	0.6-3.2	
739	ZENANTRKSSR	10.89>50		
740	ZSNPRGRRHPG	12.40	5.9-29	
741	ZENANT	3.75	>50	
742	ZANTRKS	11.05	>50	
743	ZTRKSS	12.11	13->50	
744	ZRKSSR	11.05	>50	
745	ZKSSRSN	11.05	40-48	
746	ZSSRSNPG	10.04	>50	
747	ZRSNPRG	12.40	>50	
748	ZSNPRG	10.04	>50	
749	ZPRGRRH	12.40	11-20	
750	ZRRHPG	12.10	30	
751 (HepC core)	ZKSSRGN	12.40	>50	
752 (HepC p26664)	ZKTSEERSQPRGRRQPG	12.10	9.8	1.6
753	ZTrKSSrSNPrGrRHPG			1.6
754	ZTRKSSrSNPRGrRHPG			
721 (HAX42) SDHALGTLNLRSDNAKEPGDYNCCGNSTGRKVFNRRRPSAIFT		11.27	1.7	

FIG. 10A

Peptide Name	Sequence	pI	Σ_{50}	GST/C2BBe1
ELAN018 (PAX2)	1 STPPSREAYSRPYSVVDSDDTNAKHSNSHNRRLTRSRPNC 10 SRPYSVDDSDTNAKHSNSHNR 20 STPPSREAYSRPYSVVDSDS 30 TNAKHSSNRLRTRSRPN 40 TNAKHSSHNN	10.88 0.6-0.9. 1	+++ - - ++	-
104				+/-
105				-
106				-
113				-
114	SSHNRRLRTR			+/-
115	RRLRTRSRPN			+/-
Z32	ZTNAKHSSHNRRLRTRSRPN	12.7	1.2	
Z33	ZTNAKHSSHNRRLRTR	12.58	1.6	
Z34	ZSSHNRRLRTRSRPN	12.7	1.6.	1.5
Z35	ZSSHNRRLRTR	12.58	0.38 - 1.8	2.7
Z26	ZSEANLDGRKSRYSSPRRNISSTRPRTSPNSVHARYPSTDHD	10.88	7-8, 3	
Z38	ZSRANTDGRKSRYSSPRRNISSTEPLSPNSVHARYPSTDHD	10.88	1.7. 0.9	
Z55	ZTNAKHSSHNN		42	
Z56	ZRRRLRTRSRPN			1.7
Z57	ZRRRLRTRSRP			1.9
Z58	ZRRRLTR			
Z59	ZrrlTrSrPN			NOT DONE
Z73	ZASHNRRLRTR			1.5. 5.5
Z74	ZSAHNRRRLRTR			6.2
Z75	ZSSANRRLRTR			1.6
Z76	ZSSHARRRLRTR			1.8
Z77	ZSSHNARLRTTR			3.9.
Z78	ZSSHNRALRTR			5.2
Z79	ZSSHNRRARTR			4.5, 4.6
Z80	ZSSHNRRLLATR			1.4
Z81	ZSSHNRRRLRAR			3.4, 5.2
Z82	ZSSHNRRRLRTA			2.2
Z21 (HAX42)	ZSDHALGNTNLRSDNAKEPGDYNCCNGNSTGRKVFNRRRPSAIPT	11.27	0.7	

FIG. 1 OB



Docket No.: 1101-209-999

Serial No.: 09/079,819

Inventor(s): ALVAREZ et al.

Title: "RANDOM PEPTIDES THAT BIND TO GASTROINTESTINAL
TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS"

<u>Peptide Name</u>	<u>Sequence</u>	<u>pI</u>	<u>IC₅₀</u>	<u>GST/C2B8e1</u>
ELAN016 (SNi10) 116	1 10 20 30 40 RVGQCTDSDVRRPWARS CAHQGCCAGTRNSHGCITRPLRQASAH			++
117	RVGQCTDSDVRRPWARS CAHQGCCAGTRNSHGCITRPLRQASAH			-
118	GTRNSHGCITRPLRQASAH			+
Z17	ZRVGQCTDSDVRRPWARS CAHQGCCAGTRNSHGCITRPLRQASAH	8.66	3.6	+/-
Z16C23	ZCGAGTRNSHGCITRPLRQASAH	9.03	0.7	
Z36	ZVRPWARS CAHQGCCAGTRNS	11.62	0.27	
Z37	ZCTDSDVRRPWARS C	8.01	3	
<u>Peptide Name</u>	<u>Sequence</u>	<u>pI</u>	<u>IC₅₀</u>	<u>GST/C2B8e1</u>
ELANO21 (HAX42) ELANO18 (PAX2)	1 10 20 30 40 SDHALGTNLRSNAKEPGDYNCGGGNSTGRKVFNRRRPSAIP			++
	STPPSREAYSRPVSDSDSDTNAKHSSHNRLRTRSRPN	11.27	5.5	+++
Z26	ZSEANLDGRKSRYSSPRNSSTRPRTSPNVS HARYPSTDHD	10.88	0.23	
Z38	ZSRANTDGRKSRYSSPRNSSTEPRLS PNSV HARYPSTDHD	10.88	<0.2	
Z34 (PAX2 14mer)	ZSSHNRLRTRSRPN	12.7	0.33	

FIG. 1 OC

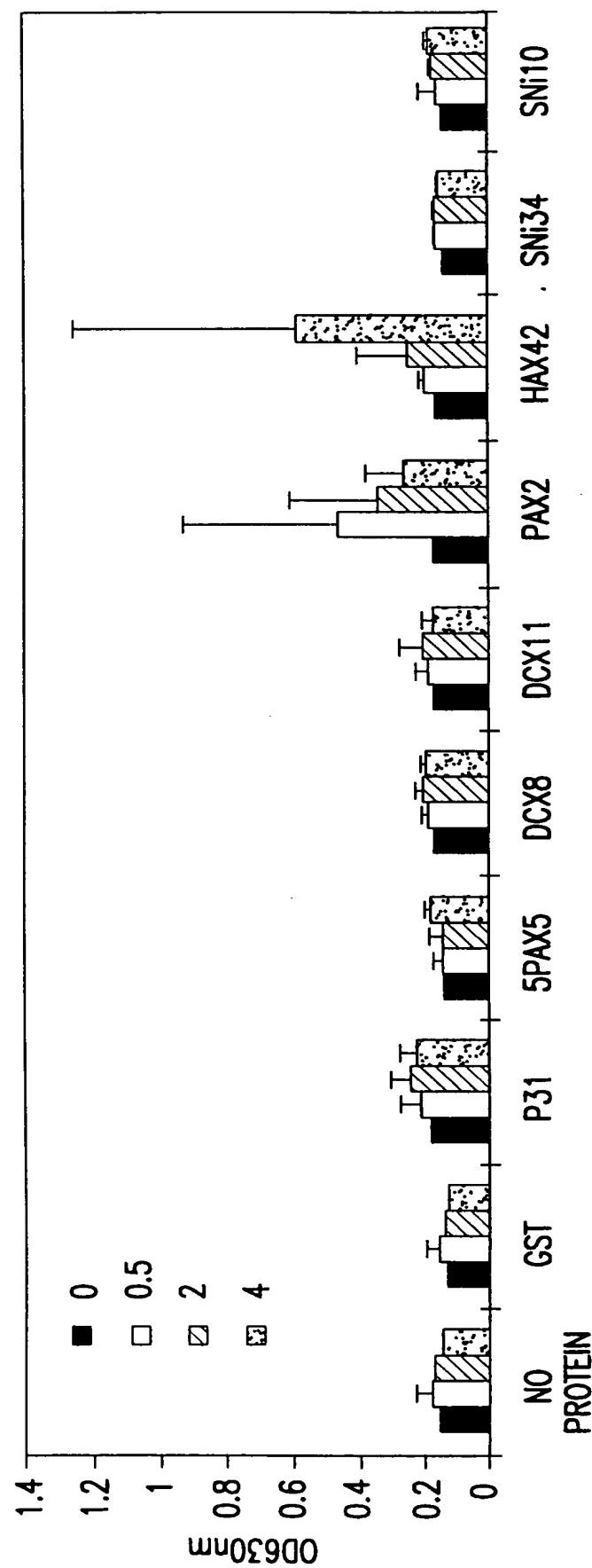


FIG. 11A

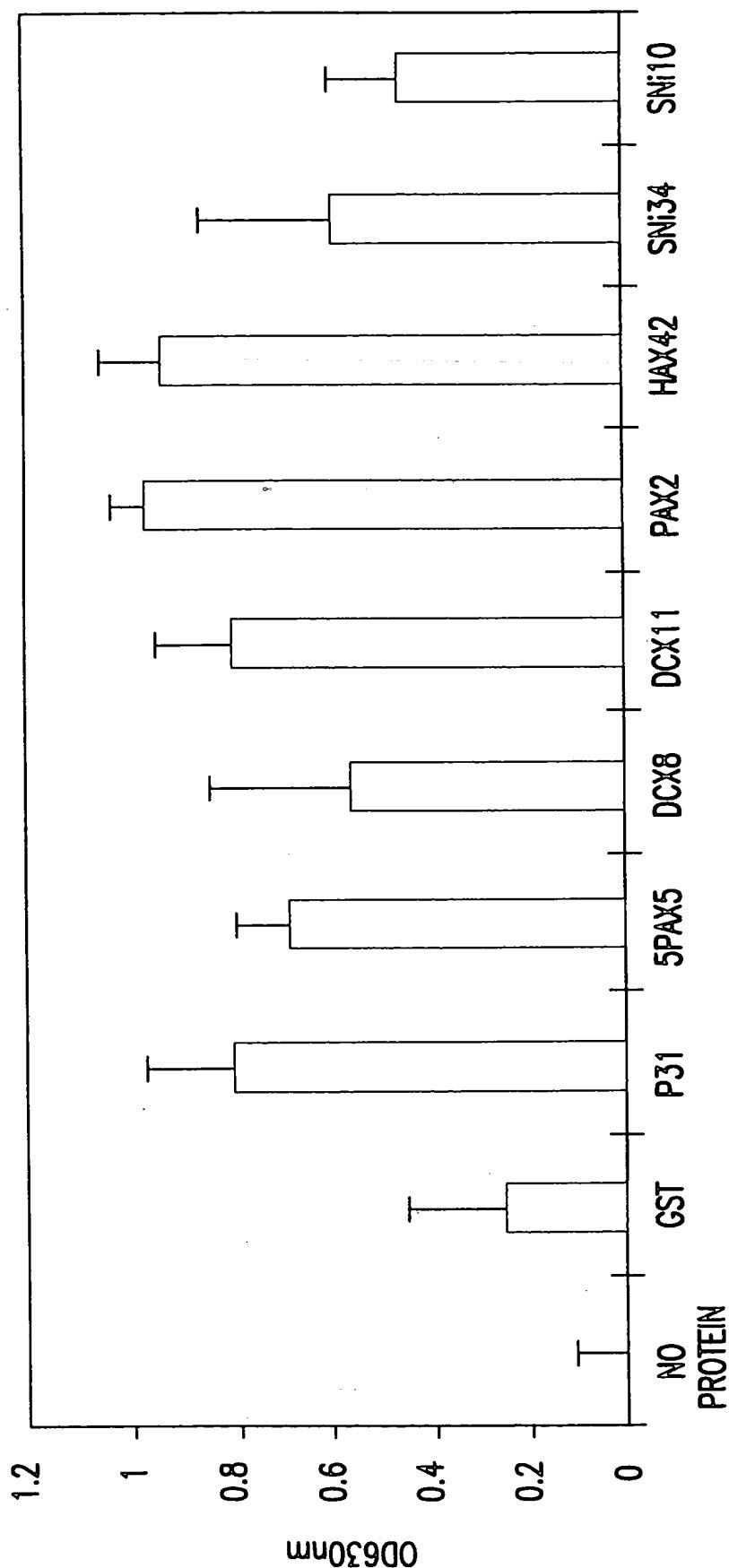


FIG. 11B

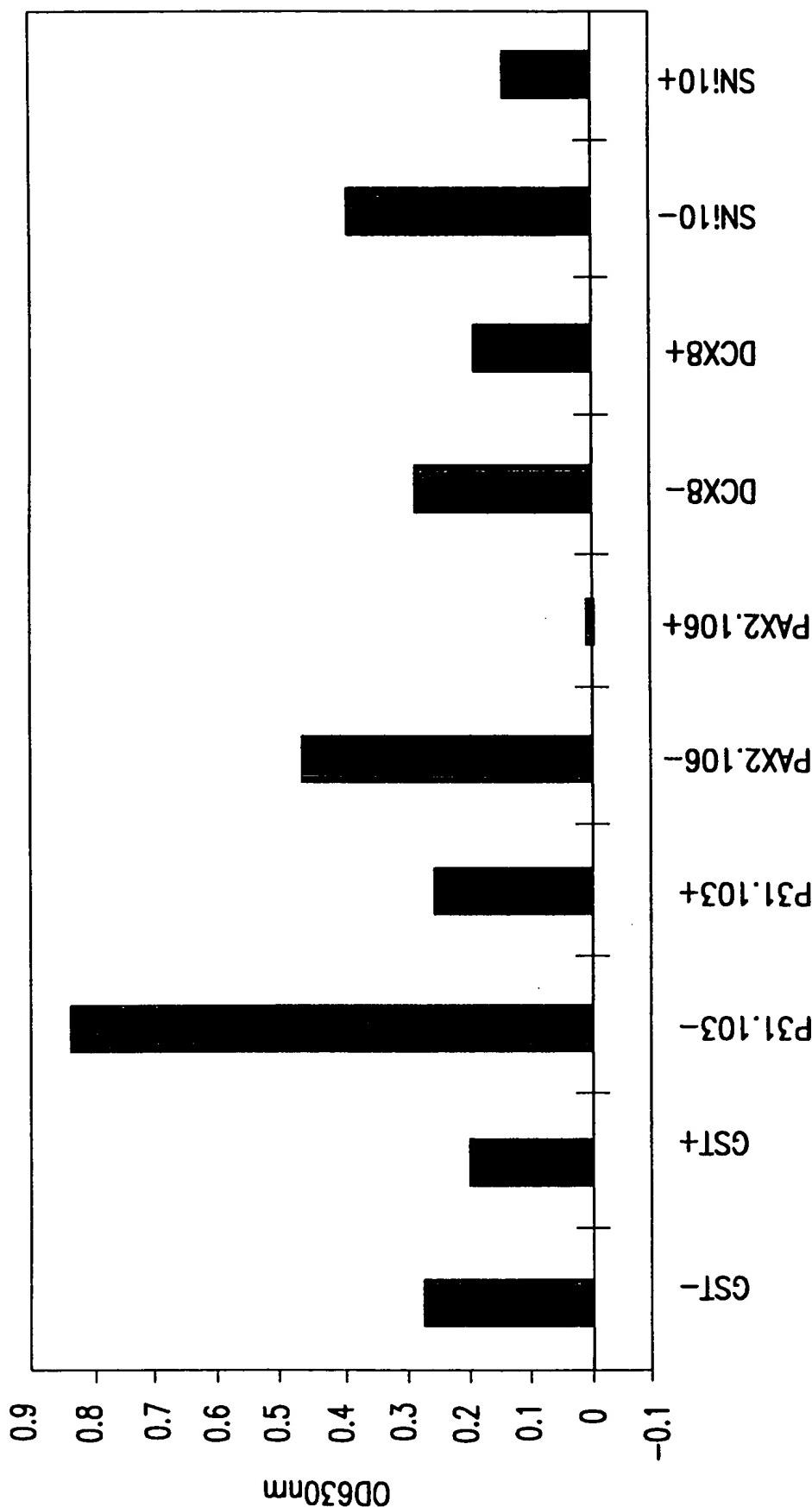


FIG. 12

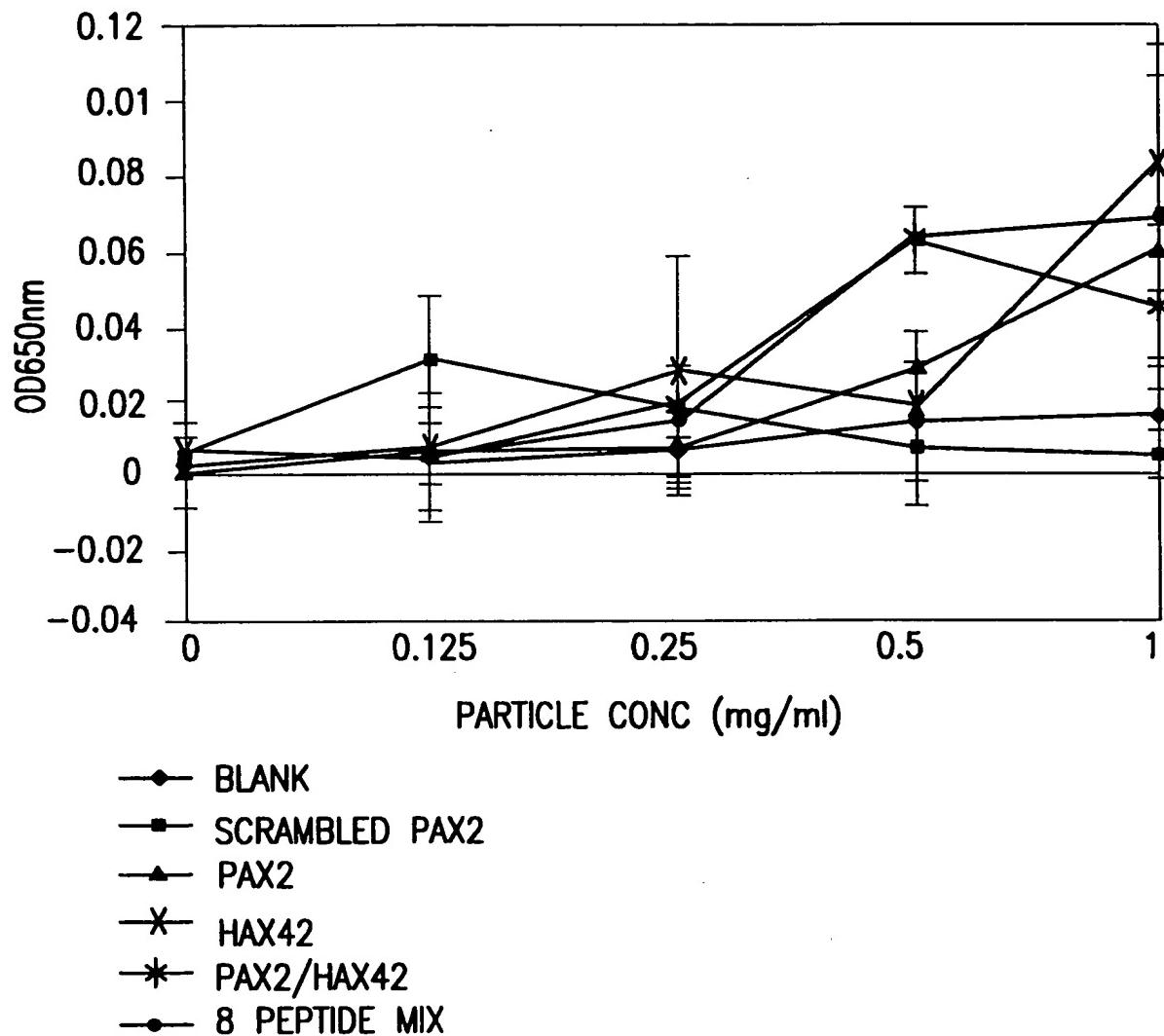


FIG.13A

APPENDIX
DRAFTS

10
CLASS

Docket No.: 1101-209-999

Serial No.: 09/079,819

Inventor(s): ALVAREZ et al.

Title: "RANDOM PEPTIDES THAT BIND TO GASTROINTESTINAL
TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS"

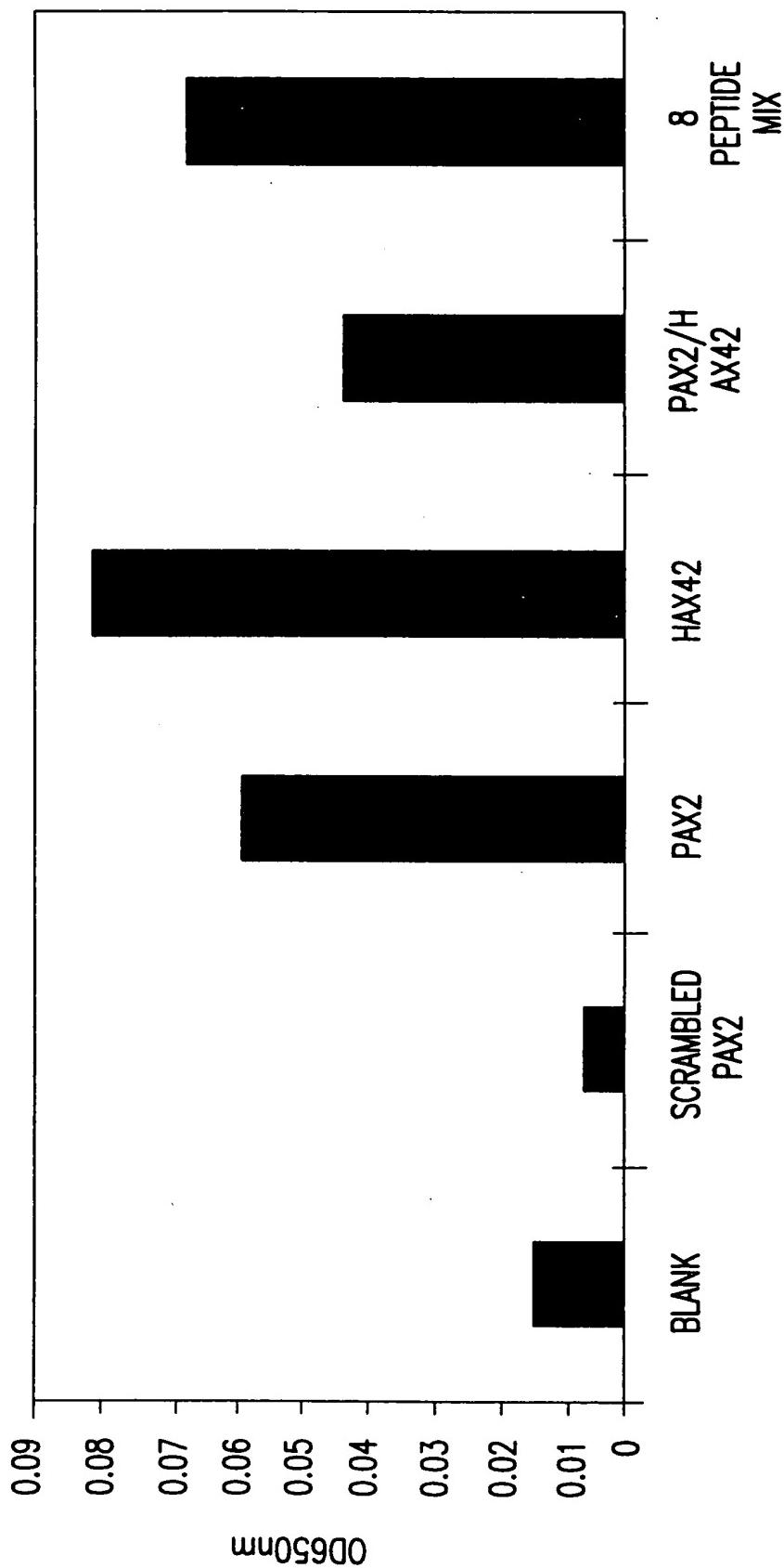


FIG. 13B

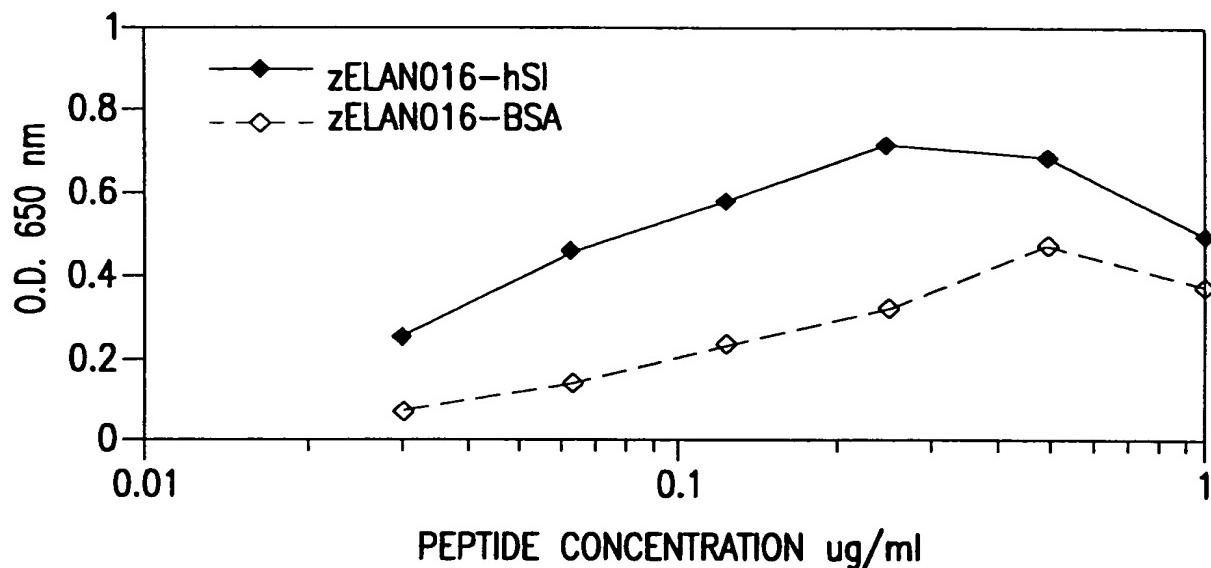


FIG. 14A

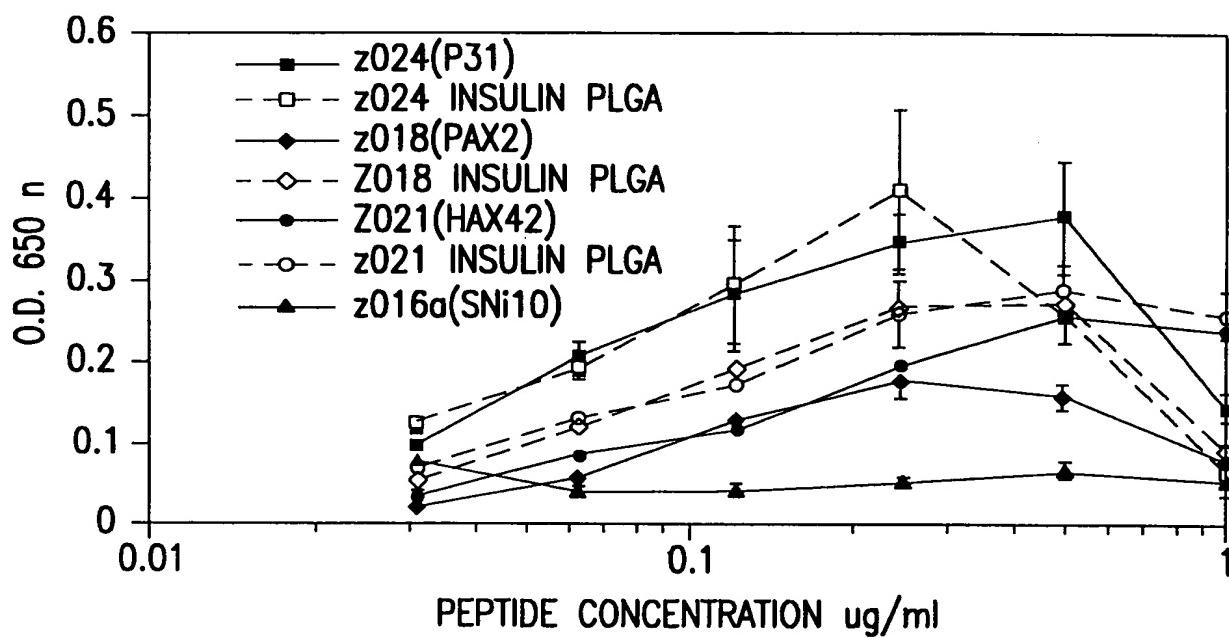


FIG. 14B

100
FIRST CLASS

Docket No.: 1101-209-999
Serial No.: 09/079,819
Inventor(s): ALVAREZ et al.
Title: "RANDOM PEPTIDES THAT BIND TO GASTROINTESTINAL
TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS"

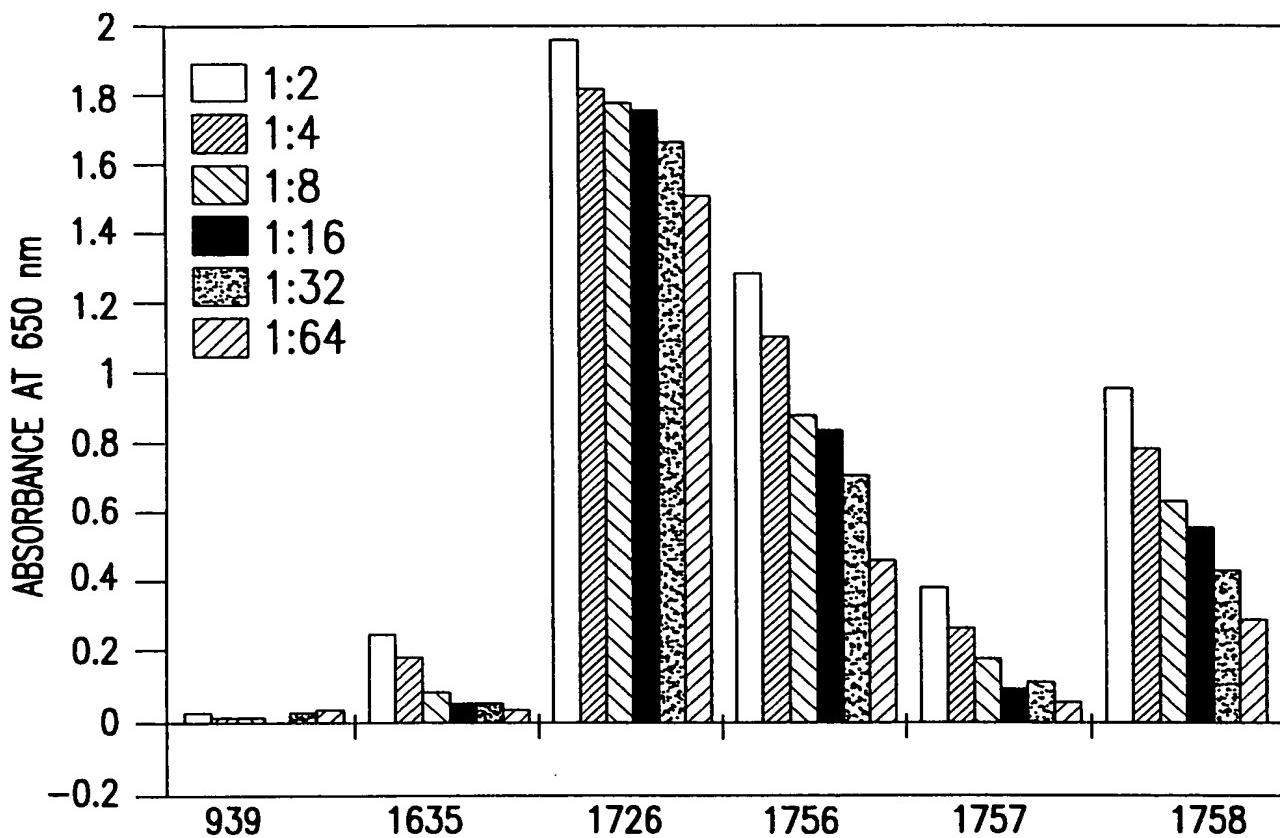


FIG. 15A

DRAFTED

10
CLASS

Docket No.: 1101-209-999

Serial No.: 09/079,819

Inventor(s): ALVAREZ et al.

Title: "RANDOM PEPTIDES THAT BIND TO GASTROINTESTINAL
TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS"

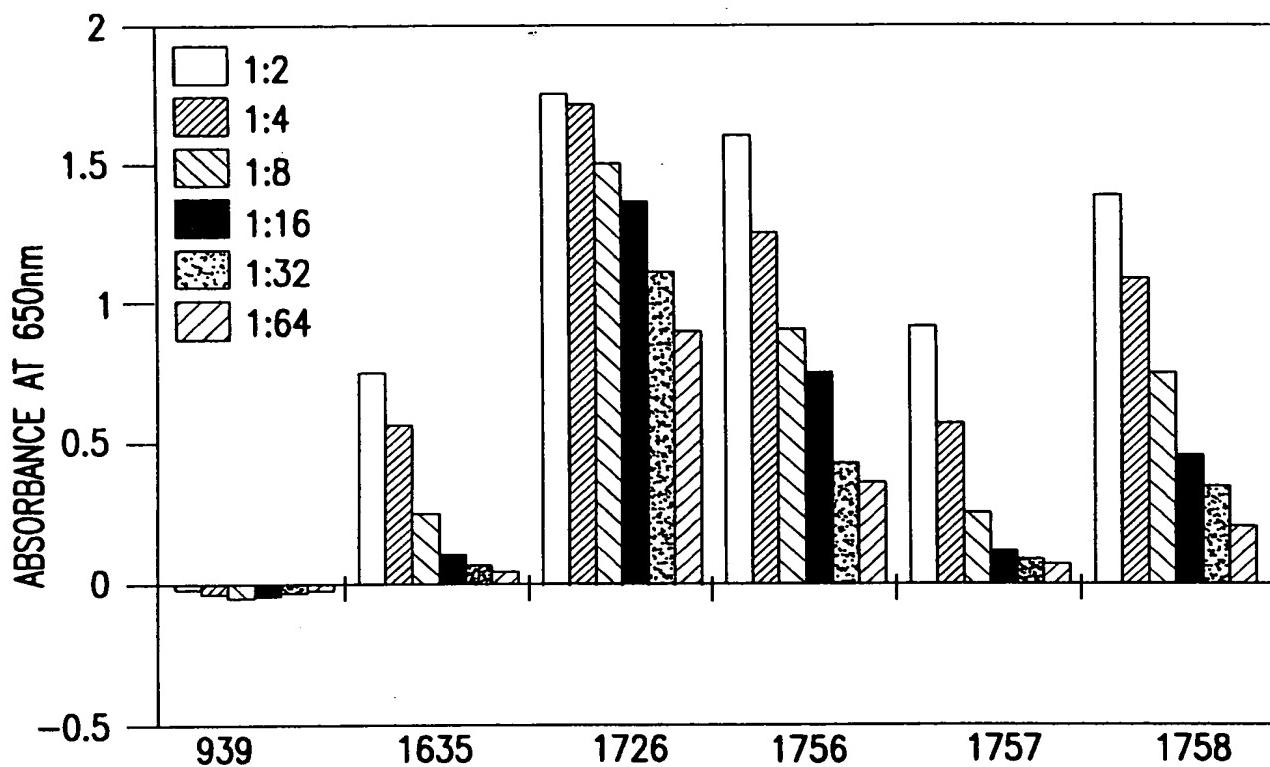


FIG. 15B

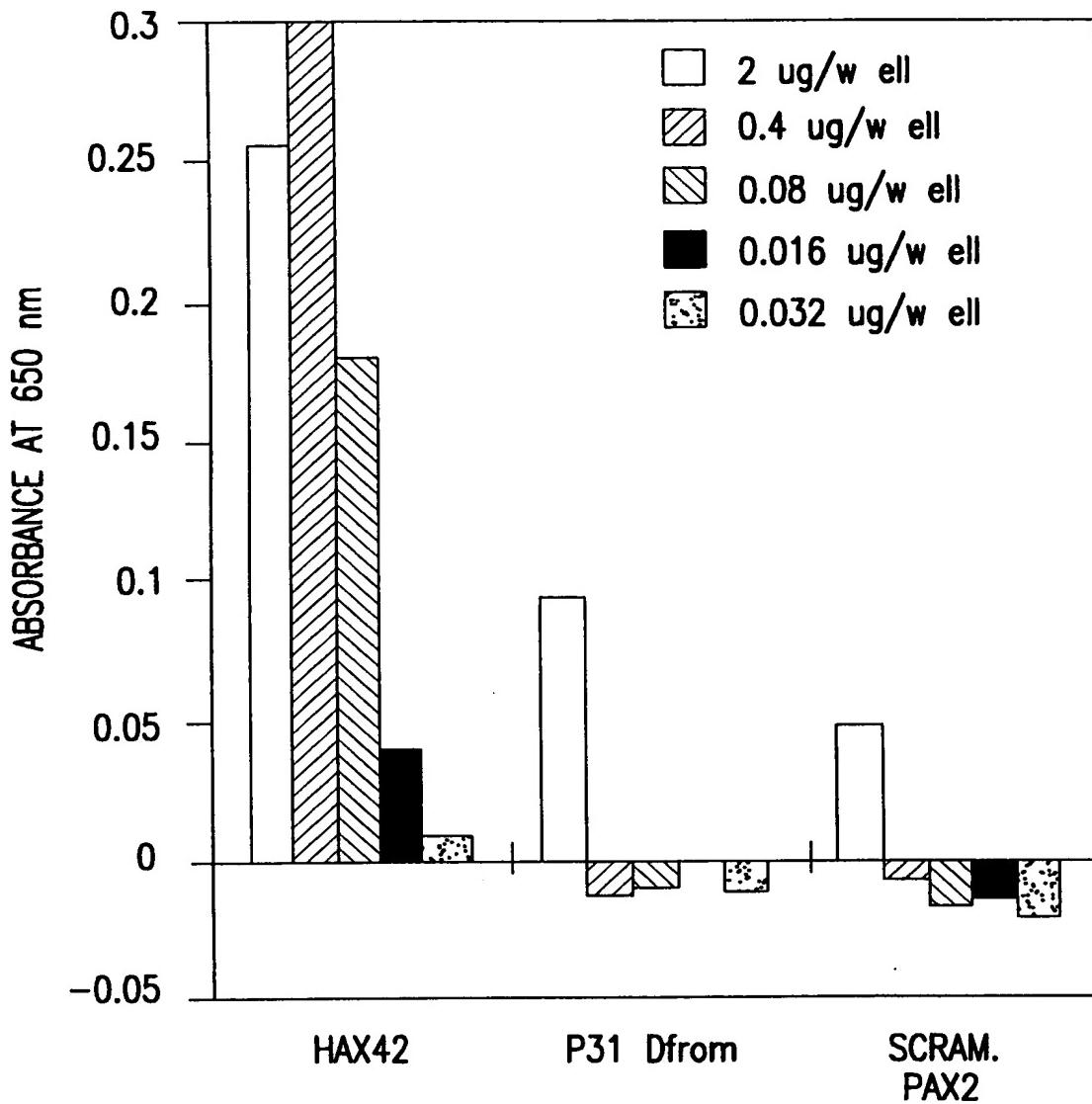


FIG.16A

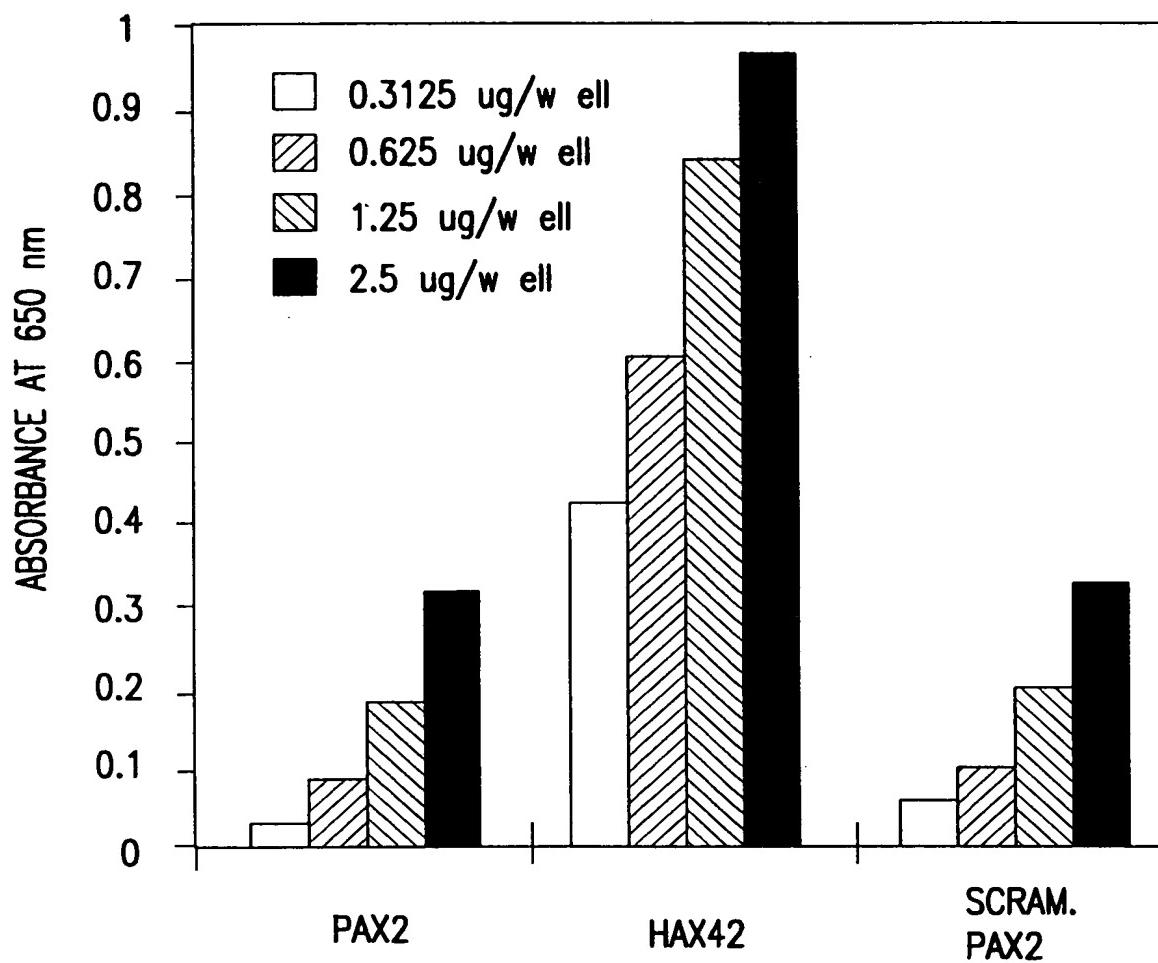


FIG.16B

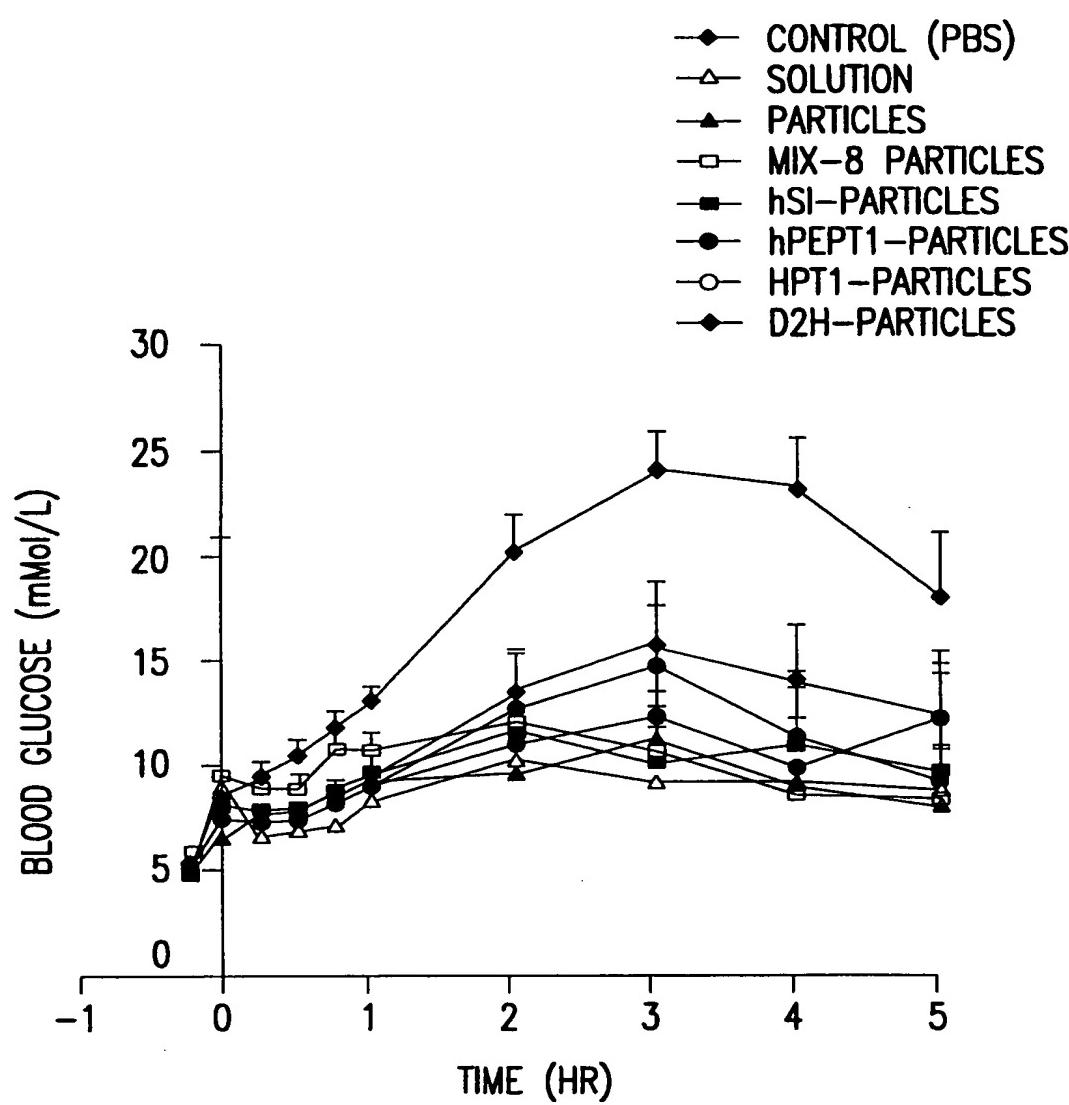


FIG. 17A

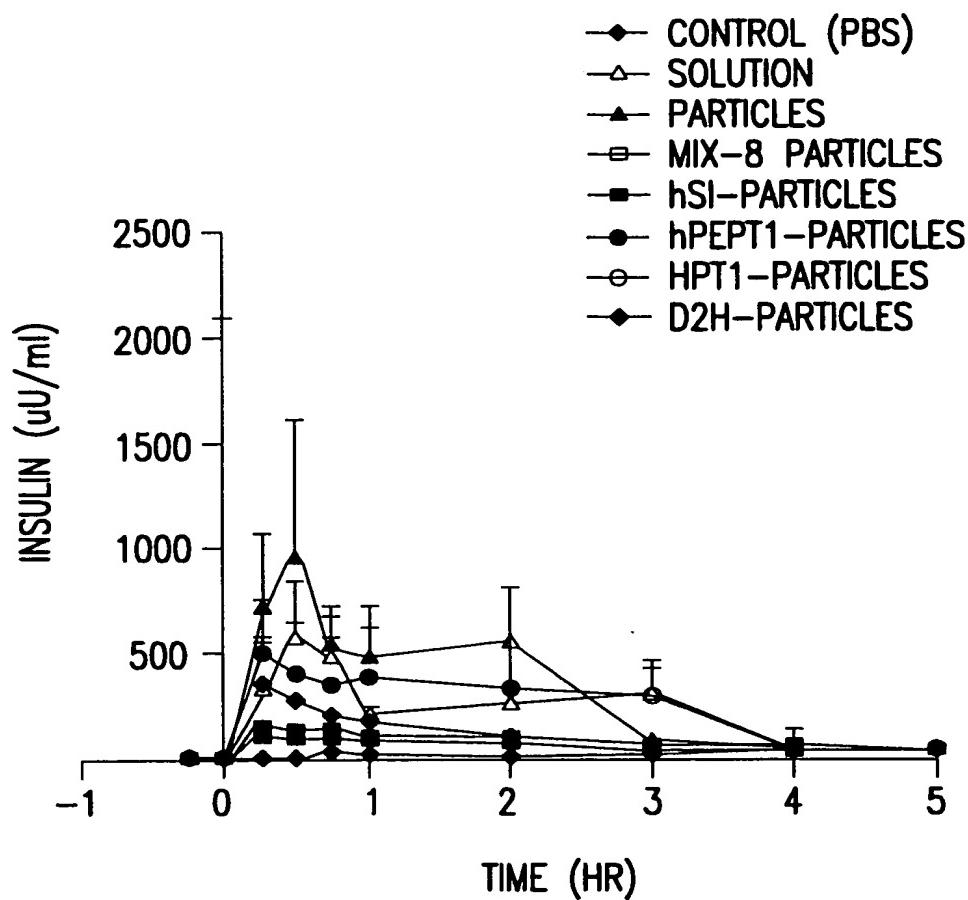


FIG. 17B

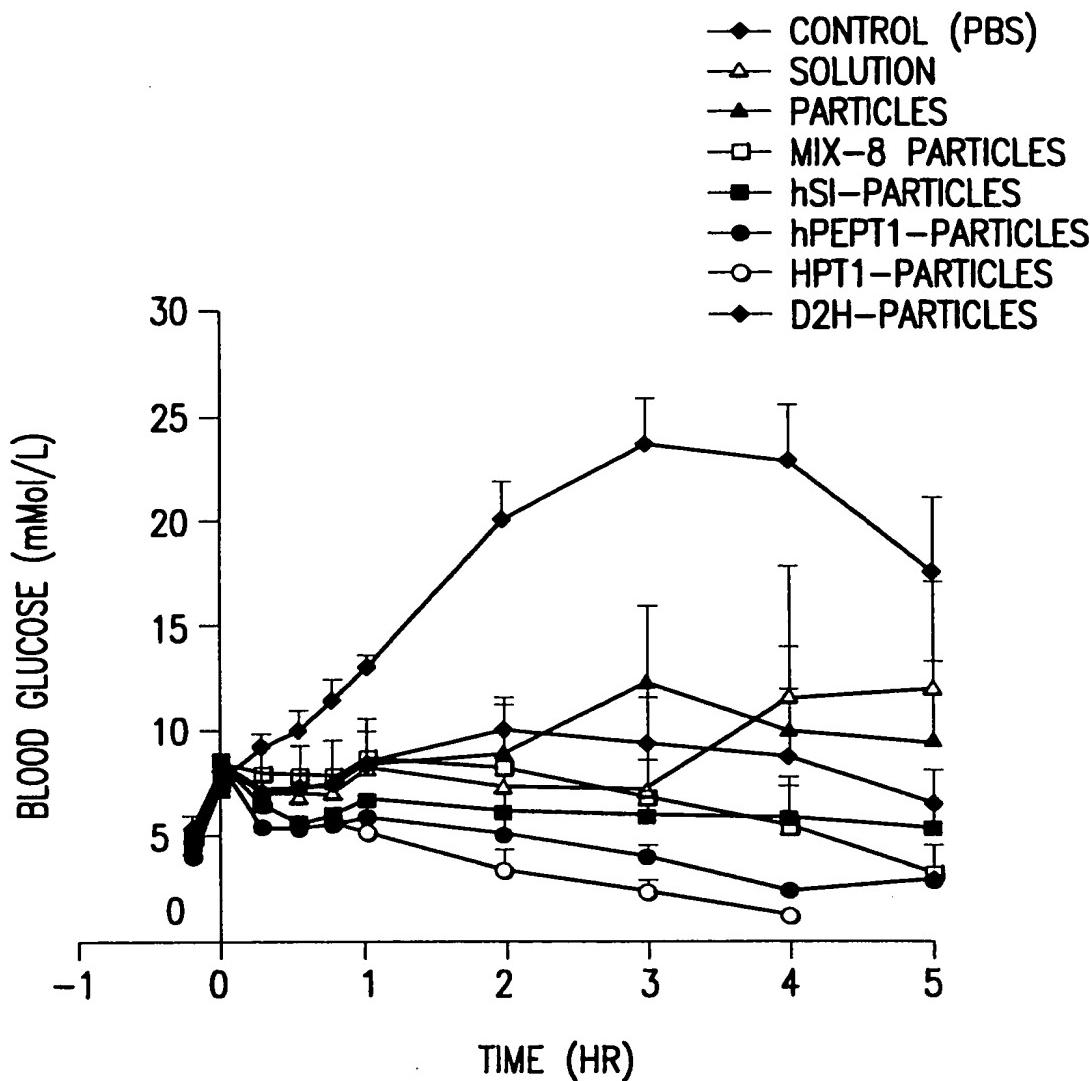


FIG. 18A

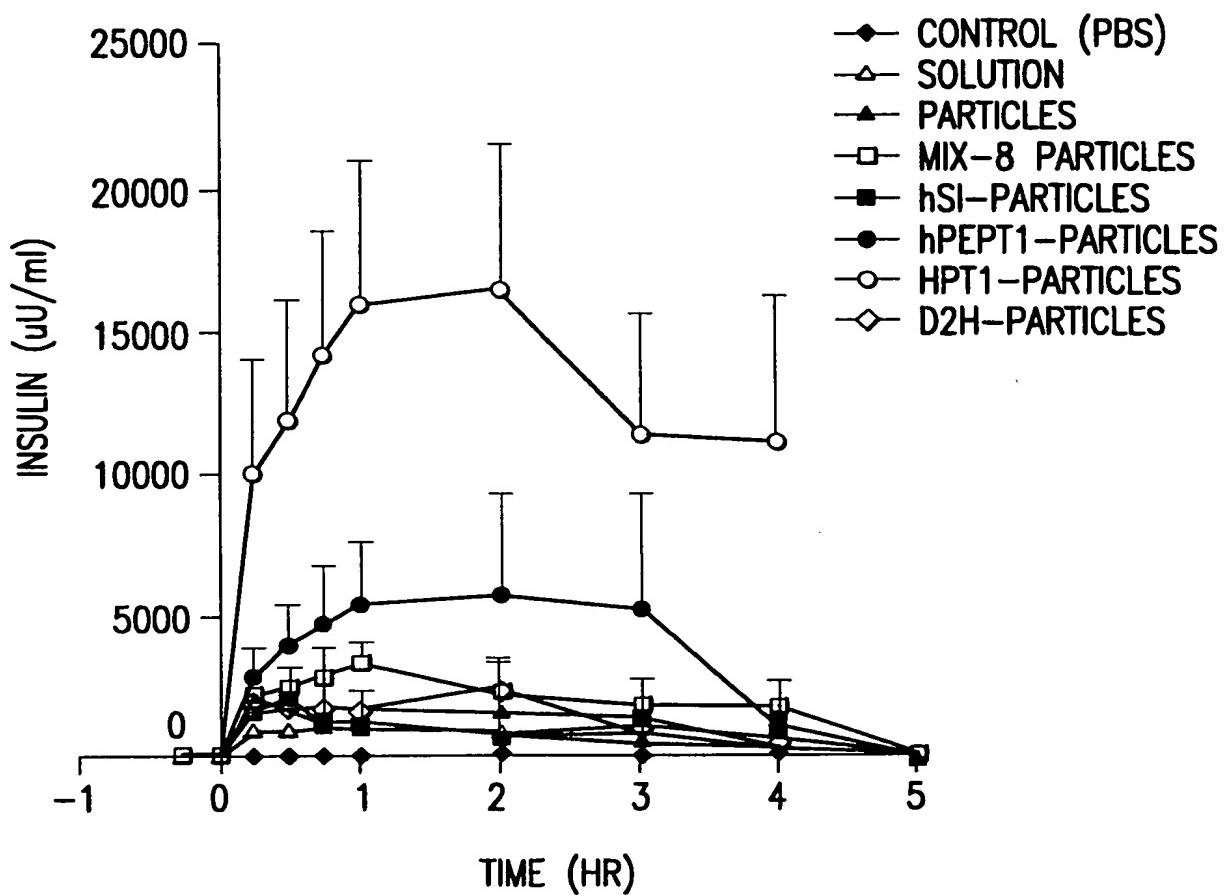


FIG. 18B

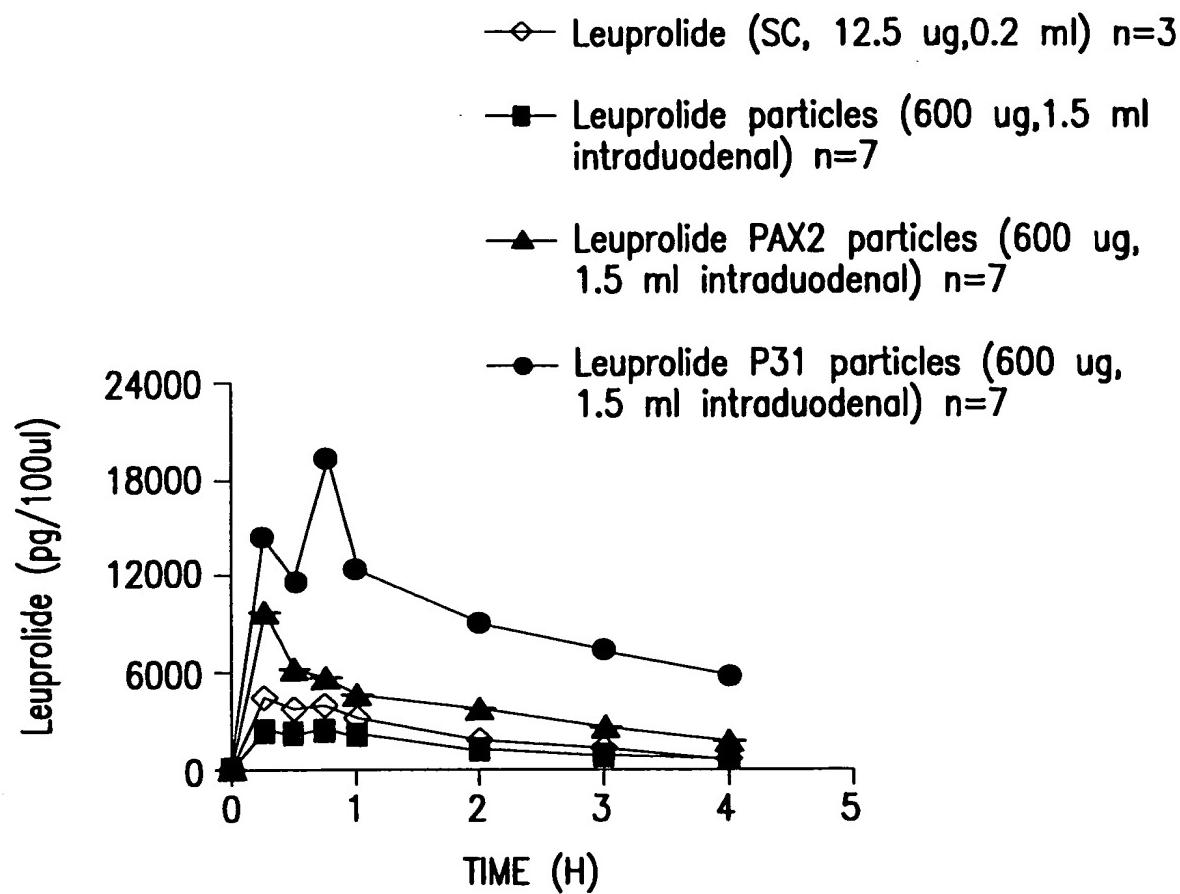


FIG. 19

Docket No.: 1101-209-999

Serial No.: 09/079,819

Inventor(s): ALVAREZ et al.

Title: "RANDOM PEPTIDES THAT BIND TO GASTROINTESTINAL
TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS"

P31 AA SEQ. POSITION	KNOWN PROTEIN	HOMOLOGOUS SEQ. POSITION
12-34	FASCICULIN 2	10-32
4-12	MESENTERICOPEPTIDASE	54-62
15-31		175-191
26-39	CORE PROTEIN (HEPATITIS C VIRUS)	5-18
26-39		11-24
26-39		21-34
26-39		38-51
23-30		39-55
25-39		41-55
26-39		51-64
16-39	PT-NANBH POLYPROTEIN N-TERMINUS	51-64
28-40	AL2 PROTEIN (CAENORHABDITISELEGANS)	70-82
26-38	CAPSID PROTEIN (HEPATITIS C VIRUS TYPE 3g)	48-60
26-39	GENOME POLYPROTEIN (HEPATITIS C VIRUS)	57-70

FIG.20

DCX8AA SEQ. POSITION	KNOWN PROTEIN	HOMOLOGOUS SEQ. POSITION
20-27	ENDO-1,4-BETA-D-GLUCANASE	78-85
30-37		221-228
21-34	P-HYDROXYBENZOATE HYDROXYLASE	285-298
5-15		54-64
7-21	CYTOCHROME	50-64
7-21	CYTOCHROME C3	50-64
	TRIMETHYLARNINE DEHYDROGENASE	208-219
32-43		396-407
30-37	Gag-JunD FUSION PROTEIN	24-31
26-30		16-20
23-44	SECRETIN PRECURSOR, N-PROSECRITIN, SECRITIN AMIDE	18-39
33-44	T-CELL RECEPTOR V BETA CHAIN	15-26
27-33		3-9
23-44	SECRETIN PRECURSOR PIR	18-39
31-44	HYPOTHETICAL PROTEIN V (SYNECHOCYSTIS)	275-288
24-30		251-257
23-43	PUTATIVE RNA BINDING PROTEIN	230-250
28-40	Mu SON OF SEVENLESS 1	1-13
24-35	NEUROPEPTIDE PRECURSOR	80-91
29-43		5-19
23-43	RNA-BINDING PROTEIN (MACACAFASCICULARIS)	230-250
23-43	RNA-BINDING PROTEIN (HOMOSAPIENS)	230-250
23-43	AUTOSOMAL GENE-AZOOSPERMIA FACTOR	230-250
25-38	COLLAGEN	25-28
24-35		4-15
29-41	PROBABLE CELL GROWTH REGULATOR	306-318
24-35	RIBOSOMAL PROTEIN S2	24-35
T6-39		182-185
24-44	CAENORHABDITIS ELEGANS	296-316
23-34	pid:e208155 (HOMO SAPIENS)	61-72
36-43		116-123

FIG.21A

DCX8A SEQ. POSITION	KNOWN PROTEIN	HOMOLOGOUS SEQ. POSITION
24-38	XYLULOSE KINASE	16-30
24-39	CAENORHABDITIS ELEGANS	57-72
26-42		65-81
27-33	HYPOTHETICAL PROTEIN-PHAGE BZ13	22-28
35-39		31-35
30-42	CEREBELLIN-LIKE GLYCOPROTEIN	2-14
8-22	DNA PRIMASE	170-184
2-7		76-81
5-21	COAT PROTEIN (BEAN COMMON MOSAIC VIRUS)	12-28
5-21	COAT PROTEIN (BEAN COMMON MOSAIC VIRUS)	33-49
5-21		19-35
5-21	POLYPROTEIN (BEAN COMMON MOSAIC VIRUS)	215-231
5-21		39-55
5-21	Nib PROTEINCOAT PROTEIN (COWPEA APHID-BOME MOSAIC VIRUS)	92-108
2-13	MHC CLASS 1 PIP1 (PITHECIA)	111-122
14-22		236-334
3-19	TALIN (CAENORHABDITIS ELEGANS)	1538-1554
2-9	ACETAMIDASE PIR	359-366
9-20		483-494
10-16	RHIZOBIONS ETLI STRAIN	134-140
17-30		173-186
31-39		200-208
2-11	NEUROTOXIN 1 (TOXIN B) A. STOKESI	7-16
12-33		26-47
21-27	SUID HERPES VIRUS 1 EARLY PROTEIN	425-432
30-43		51-64
13-42	RICE cDNA PARTIAL SEQUENCE	50-151
8-15	FUSION PROTEIN	24-31
4-8		16-20
1-22	SECRETIN PRECURSOR, N-PROSECRETIN, SECRETIN-AMIDE	18-39
11-22	T-CELL RECEPTOR V BETA CHAIN	15-26
5-11		3-9
9-22	HYPOTHETICAL PROTEIN	275-288
2-8		251-257

FIG.21B

DCX8A SEQ. POSITION	KNOWN PROTEIN	HOMOLOGOUS SEQ. POSITION
1-21	PUTATIVE RNA BINDING PROTEIN	230-250
6-18	HYPOTHETICAL PROTEIN-MOUSE PIR	1-13
2-13	NEUROPEPTIDE PRECURSOR	80-91
7-21	orf3-HUMAN	5-19
1-21	RNA-BINDING PROTEIN	230-250
13-16	COLLAGEN	25-28
7-19	PROBABLE CELL GROWTH OR DIFFERENTIATION REGULATOR	306-318
2-13	RIBOSOMAL PROTEIN S2	14-25
14-17		182-185
2-22	CAENORHABDITIS ELEGANS	296-316
1-12	HOMOSAPIENS	61-72
14-21		116-123
2-16	XYLULOSE KINASE	16-30
8-15	T CELL RECEPTOR DELTA CHAIN	55-62
5-8		12-15
8-17	SEQ. 43 FROM PATENT US	12-21

FIG.21C

DAB10 AA SEQ. POSITION	KNOWN PROTEIN	HOMOLOGOUS SEQ. POSITION
13-34	1,3-BETA-GLUCANASE	231-252
3-11	PHOTOSYNTHETIC REACTION CENTER	20-28
16-27		128-139
28-35	MYB PROTO-ONCOGENE PROTEIN	131-138
5-18		32-45
23-36	LYSOZYME MUTANT	130-143
28-35	LIPASE	400-407
3-15		159-171
3-37	TRYPSIN	169-203
13-34	1,3-1,4-BETA-GLUCANASE	232-253
4-10	LACTATE DEHYDROGENASE	190-196
11-7		244-250
4-10	APO-LACTATE DEHYDROGENASE	190-196
11-17		244-250
4-10	LACTATE DEHYDROGENASE	191-197
11-17		245-251
16-26	OVTORNSFERRIN	240-250
23-36	GENOME POLYPROTEIN MATRIX PROTEIN	1022-1035
14-20	ROUS SARCOMA VIRUS	43-49
2-12		13-23
14-20	HYPOTHETICAL PROTEIN-AVIAN LEUKOSIS VIRUS	43-49
4-20	T CELL RECEPTOR DELTA CHAIN VARIABLE REGION	1-4
14-18		12-16
2-12	GAG POLYPROTEIN-AVIAN ENDOGENOUS VIRUS RAV-0	139-149
14-20		169-175
	p19 PROTEIN-AVIAN ERYTHROBLASTOSIS VIRUS	189-199
14-20		219-225
7-19	ALI PROTEIN-POTATO YELLOW MOSAIC VIRUS	222-234
3-22	ENDO-1,4-BETA GLUCANASE	186-205
6-18	I _a PROTEIN-BROME MOSAIC VIRUS	430-442
2-12	GAG POLYPROTEIN-FUJINAMI SARCOMA VIRUS	186-196
14-22		216-222
2-12	GAG PROTEIN-ROUS SARCOMA VIRUS	190-200
14-20		220-226
1-12	CORTICOTROPIN-LIKE INTERMEDIATE LOBE PEPTIDE	7-18
1-22	GENE PRODUCT (CAENORHABDITIS ELEGANS)	4-25
31-37	T CELL RECEPTOR DELTA CHAIN	56-62
26-39		12-15
26-37	LYSOZYME MUTANT	133-144

FIG.22

Title: "RANDOM PEPTIDES THAT BIND TO GASTROINTESTINAL
TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS"

ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro 1 5 10 15	48
ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30	96
TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 40 45	144
GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT GAT GTT AAA Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys 50 55 60	192
TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80	240
ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95	288
GGA GCG GTT TTG GAT ATT AGA TAC GGT GTT TCG AGA ATT GCA TAT AGT Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110	336
AAA GAC TTT GAA ACT CTC AAA GTT GAT TTT CTT AGC AAG CTA CCT GAA Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125	384
ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA ACA TAT TTA AAT Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140	432
GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG TAT GAC GCT CTT GAT Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160	480
GTT GTT TTA TAC ATG GAC CCA ATG TGC CTG GAT GCG TTC CCA AAA TTA Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175	528
GTT TGT TTT AAA AAA CGT ATT GAA GCT ATC CCA CAA ATT GAT AAG TAC Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190	576
TTG AAA TCC AGC AAG TAT ATA GCA TGG CCT TTG CAG GGC TGG CAA GCC Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205	624
ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT CTG GTT CCG CGT Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220	672
GGA TCC CCA GGA ATT CCC GGG TCG ACT CGA GCG GCC GCA TCG TGA Gly Ser Pro Gly Ile Pro Gly Ser Thr Arg Ala Ala Ala Ser 225 230 235	717

FIG.23